

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 3, 2004, 03:36:17 ; Search time 361 Seconds
(without alignments)
3098.044 Million cell updates/sec

Title: US-10-063-732-120
Perfect score: 1172
Sequence: 1 MATHALEIAGLFLGGVGMGV.....QKSYHTGKKSPSVYRSQYV 225

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delopt 6.0 , Delext 7.0

Searched: 3267054 seqs, 2485319735 residues

Total number of hits satisfying chosen parameters: 6534108

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US10063732/runat.01092004.155518.20479/app.query.fasta_1.391
-DB=Published_Applications NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosu62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10063732@cgn 1 1 354 @runat.01092004.155518.20479
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/PCRUS_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*

14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
*					

c	1	1172	100.0	678	15	US-10-029-386-22722	Sequence 22722, A
	2	1172	100.0	1793	9	US-09-731-872-164	Sequence 164, App
	3	1172	100.0	1793	10	US-09-876-997-164	Sequence 164, App
	4	1172	100.0	2010	10	US-09-946-374-327	Sequence 327, App
	5	1172	100.0	2010	12	US-10-015-395A-327	Sequence 327, App
	6	1172	100.0	2010	13	US-10-206-915-357	Sequence 357, App
	7	1172	100.0	2010	13	US-10-199-670-357	Sequence 357, App
	8	1172	100.0	2010	13	US-10-201-858-357	Sequence 357, App
	9	1172	100.0	2010	13	US-10-205-890-357	Sequence 357, App
	10	1172	100.0	2010	13	US-10-208-024-357	Sequence 357, App
	11	1172	100.0	2010	13	US-10-201-853-357	Sequence 357, App
	12	1172	100.0	2010	13	US-10-063-745-119	Sequence 119, App
	13	1172	100.0	2010	13	US-10-063-512-119	Sequence 119, App
	14	1172	100.0	2010	13	US-10-063-513-119	Sequence 119, App
	15	1172	100.0	2010	13	US-10-063-549-119	Sequence 119, App
	16	1172	100.0	2010	13	US-10-063-569-119	Sequence 119, App
	17	1172	100.0	2010	13	US-10-063-551-119	Sequence 119, App
	18	1172	100.0	2010	13	US-10-174-581-357	Sequence 357, App
	19	1172	100.0	2010	13	US-10-176-483-357	Sequence 357, App
	20	1172	100.0	2010	13	US-10-176-749-357	Sequence 357, App
	21	1172	100.0	2010	13	US-10-176-914-357	Sequence 357, App
	22	1172	100.0	2010	13	US-10-176-915-357	Sequence 357, App
	23	1172	100.0	2010	13	US-10-006-485A-327	Sequence 327, App
	24	1172	100.0	2010	13	US-10-013-907A-327	Sequence 327, App
	25	1172	100.0	2010	13	US-10-015-499A-327	Sequence 327, App
	26	1172	100.0	2010	13	US-10-063-555-119	Sequence 119, App
	27	1172	100.0	2010	13	US-10-063-563-119	Sequence 119, App
	28	1172	100.0	2010	13	US-10-063-594-119	Sequence 119, App
	29	1172	100.0	2010	13	US-10-063-553-119	Sequence 119, App
	30	1172	100.0	2010	13	US-10-063-554-119	Sequence 119, App
	31	1172	100.0	2010	13	US-10-176-484-357	Sequence 357, App
	32	1172	100.0	2010	13	US-10-180-550-357	Sequence 357, App
	33	1172	100.0	2010	13	US-10-183-014-357	Sequence 357, App
	34	1172	100.0	2010	13	US-10-187-738-357	Sequence 357, App
	35	1172	100.0	2010	13	US-10-187-740-357	Sequence 357, App
	36	1172	100.0	2010	13	US-10-187-883-357	Sequence 357, App
	37	1172	100.0	2010	13	US-10-194-363-357	Sequence 357, App
	38	1172	100.0	2010	13	US-10-194-460-357	Sequence 357, App
	39	1172	100.0	2010	13	US-10-194-463-357	Sequence 357, App
	40	1172	100.0	2010	13	US-10-194-484-357	Sequence 357, App
	41	1172	100.0	2010	13	US-10-195-884-357	Sequence 357, App
	42	1172	100.0	2010	13	US-10-195-896-357	Sequence 357, App
	43	1172	100.0	2010	13	US-10-196-744-357	Sequence 357, App
	44	1172	100.0	2010	13	US-10-196-755-357	Sequence 357, App
	45	1172	100.0	2010	13	US-10-196-757-357	Sequence 357, App

ALIGNMENTS

RESULT 1
US-10-029-386-22722/c
; Sequence 22722, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 22722
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP000884.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.97
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.96
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
OTHER INFORMATION: SWISSPROT HIT: P56748, EVALUE 1.00e-120
OTHER INFORMATION: NT HIT: g14780163, EVALUE 0.00e+00
OTHER INFORMATION: EST_HUMAN HIT: AUL21779.1, EVALUE 0.00e+00
US-10-029-386-22722

Alignment Scores:
Pred. No.: 2,76e-150 Length: 678
Score: 1172.00 Matches: 225
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-10-063-732-120 (1-225) x US-10-029-386-22722 (1-678)

QY 1 MetAlaThrHisAlaLeuGluIleAlaGlyLeuPheLeuGlyValGlyMetValGly 20
Db 678 ATGGCAACCCATGCCTTAGAAATCGCTGGCTGTTTCTTGTTGGTGTGTTGGAATGGTGGGC 619
QY 21 ThrValAlaValThrValMetProGlnTrpArgValSerAlaPheIleGluAsnAsnIle 40
Db 618 ACAGTGGCTGTCACTGTCAATGCCCTCAGTGGAGAGTGTGGCTTTCATTGAAACACATC 559
QY 41 ValValPheGluAsnPheTrpGluGlyLeuTrpMetAsnCysValArgGlnAlaAsnIle 60
Db 558 GTGGTTTTTGAAAACTTCTGGGAAGGACTGTGGATGAATGGCTGAGGCAGGCTAACATC 499
QY 61 ArgMetGlnCysLysIleTyrAspSerLeuLeuAlaLeuSerProAspLeuGlnAlaAla 80
Db 498 AGGATGCAGTGCAGAAATCTATGATTCCTCGTGGCTCTTTCTCGGACCTACAGGCAGCC 439
QY 81 ArgGlyLeuMetCysAlaAlaSerValMetSerPheLeuAlaPheMetMetAlaIleLeu 100
Db 438 AGAGGACTGATGTGTGCTGCTCCGTGATGCTCTTCTTGCTTTCATGATGGCCATCCTT 379
QY 101 GlyMetLysCysThrArgCysThrGlyAspAsnGluLysValLysAlaHisIleLeuLeu 120
Db 378 GGCATGAAATGCACAGGTGCACCGGGGCAATGAGAAGGTGAAGGTCAATTCCTGCTG 319
QY 121 ThrAlaGlyIleIlePheIleIleThrGlyMetValValLeuIleProValSerTrpVal 140
Db 318 ACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGTCTCATCCCTGTGAGCTGGGT 259
QY 141 AlaAsnAlaIleIleArgAspPheTyrAsnSerIleValAsnValAlaGlnLysArgGlu 160
Db 258 GCCAATGCCATCATCAGAGATTCTATACTCAATAGTAGAATGTTGCCCAAAACGTGAG 199
QY 161 LeuGlyGluAlaLeuTyrLeuGlyTrpThrAlaLeuValLeuIleValGlyGlyAla 180
Db 198 CTTGGAGAAGCTCTCTACTTAGGATGGACCCAGGCACCTGGTGTGATGTTGGAGGAGCT 139
QY 181 LeuPheCysCysValPheCysCysAsnGluLysSerSerSerTyrArgTyrSerIlePro 200
Db 138 CTGTTCTGCTGCGTTTTTTTGTGCAACGAAAGAGCAGTAGCTACAGATACTCGATACCT 79
QY 201 SerHisArgThrThrGlnLysSerTyrHisThrGlyLysSerProSerValTyrSer 220
Db 78 TCCCATCGCACAAACCCAAAAAGTTATCACACCGGAAAGAGTACCCGAGCGTCTACTCC 19
QY 221 ArgSerGlnTyrVal 225
Db 18 AGAAGTCAGTATGTG 4

RESULT 2
US-09-731-872-164
Sequence 164, Application US/09731872
Patent No. US20020102604A1
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Bougueleret, Lydie
APPLICANT: Jobert, Severin

TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78.US3.REG
CURRENT APPLICATION NUMBER: US/09/731,872
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,629
PRIOR FILING DATE: 1999-12-08
PRIOR APPLICATION NUMBER: US 60/187,470
PRIOR FILING DATE: 2000-03-06
NUMBER OF SEQ ID NOS: 482
SOFTWARE: Patent.pm
SEQ ID NO 164
LENGTH: 1793
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 173..847
US-09-731-872-164

Alignment Scores:
Pred. No.: 1,29e-149 Length: 1793
Score: 1172.00 Matches: 225
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-10-063-732-120 (1-225) x US-09-731-872-164 (1-1793)
QY 1 MetAlaThrHisAlaLeuGluIleAlaGlyLeuPheLeuGlyValGlyMetValGly 20
Db 173 ATGGCAACCCATGCCTTAGAAATCGCTGGCTGTTTCTTGTTGGTGTGTTGGAATGGTGGGC 232
QY 21 ThrValAlaValThrValMetProGlnTrpArgValSerAlaPheIleGluAsnAsnIle 40
Db 233 ACAGTGGCTGTCACTGTCAATGCCCTCAGTGGAGAGTGTGGCTTTCATTGAAACACATC 292
QY 41 ValValPheGluAsnPheTrpGluGlyLeuTrpMetAsnCysValArgGlnAlaAsnIle 60
Db 293 GTGGTTTTTTGAAAACTTCTGGGAAGGACTGTGGATGAATGGCTGAGGCAGGCTAACATC 352
QY 61 ArgMetGlnCysLysIleTyrAspSerLeuLeuAlaLeuSerProAspLeuGlnAlaAla 80
Db 353 AGGATGCAGTGCAGAAATCTATGATTCCTCGTGGCTCTTTCTCGGACCTACAGGCAGCC 412
QY 81 ArgGlyLeuMetCysAlaAlaSerValMetSerPheLeuAlaPheMetMetAlaIleLeu 100
Db 413 AGAGGACTGATGTGTGCTGCTCCGTGATGCTCTTCTTGCTTTCATGATGGCCATCCTT 472
QY 101 GlyMetLysCysThrArgCysThrGlyAspAsnGluLysValLysAlaHisIleLeuLeu 120
Db 473 GGCATGAAATGCACAGGTGCACCGGGGCAATGAGAAGGTGAAGGTCAATTCCTGCTG 532
QY 121 ThrAlaGlyIleIlePheIleIleThrGlyMetValValLeuIleProValSerTrpVal 140
Db 533 ACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGTCTCATCCCTGTGAGCTGGGT 592
QY 141 AlaAsnAlaIleIleArgAspPheTyrAsnSerIleValAsnValAlaGlnLysArgGlu 160
Db 593 GCCAATGCCATCATCAGAGATTCTATACTCAATAGTAGAATGTTGCCCAAAACGTGAG 652
QY 161 LeuGlyGluAlaLeuTyrLeuGlyTrpThrAlaLeuValLeuIleValGlyGlyAla 180
Db 653 CTTGGAGAAGCTCTCTACTTAGGATGGACCCAGGCACCTGGTGTGATGTTGGAGGAGCT 712
QY 181 LeuPheCysCysValPheCysCysAsnGluLysSerSerSerTyrArgTyrSerIlePro 200
Db 713 CTGTTCTGCTGCGTTTTTTTGTGCAACGAAAGAGCAGTAGCTACAGATACTCGATACCT 772
QY 201 SerHisArgThrThrGlnLysSerTyrHisThrGlyLysSerProSerValTyrSer 220
Db 773 TCCCATCGCACAAACCCAAAAAGTTATCACACCGGAAAGAGTACCCGAGCGTCTACTCC 832

; PRIOR APPLICATION NUMBER: 60/105807

Alignment Scores:

Pred. No.: 1.54e-149 Length: 2010
Score: 1172.00 Matches: 225
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-063-732-120 (1-225) x US-09-946-374-327 (1-2010)

QY 1 MetAlaThrHisAlaLeuGluLeuAlaGlyLeuPheLeuGlyValGlyMetValGly 20
Db 97 ATGGCAACCCATGCCTTAGAAATCGCTGGGCTGTTTCTTGGTGGTGTGAATGGTGGGC 156

QY 21 ThrValAlaValThrValMetProGlnTrpArgValSerAlaPheIleGluAsnAsnIle 40
Db 157 ACAGTGGCTGTCACTGTCAATGCCCTCAGTGGAGAGTGTGGCCCTTCATTGAAACAACATC 216

QY 41 ValValPheGluAsnPheTrpGluGlyLeuTrpMetAsnCysValArgGlnAlaAsnIle 60
Db 217 GTGGTTTTTGAAAACTTCTGGGAAGGACTGTGGATGAATTGGTGAGGCAGGCTAACATC 276

QY 61 ArgMetGlnCysLysIleTyrAspSerLeuAlaLeuSerProAspLeuGlnAlaAla 80
Db 277 AGGATGCAGTGCAAAATCTATGATTCCTGCTGGCTCTTTCTCGGACCTACAGGCAGCC 336

QY 81 ArgGlyLeuMetCysAlaAlaSerValMetSerPheLeuAlaPheMetMetAlaIleLeu 100
Db 337 AGAGGACTGATGTGTGCTTCCGTGATGTCCTTCTTGGCTTCATGATGGCCATCCTT 396

QY 101 GlyMetLysCysThrArgCysThrGlyAspAsnGluLysValLysAlaHisIleLeuLeu 120
Db 397 GGCAATGAATGCACCAGGTGCACGGGGACAATGAGAAGTGAAGGCTCACATTCTGCTG 456

QY 121 ThrAlaGlyIleIlePheIleThrGlyMetValValLeuIleProValSerTrpVal 140
Db 457 ACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGTCTCATCCCTGTGAGCTGGGTT 516

QY 141 AlaAsnAlaIleIleArgAspPheTyrAsnSerIleValAsnValAlaGlnLysArgGlu 160
Db 517 GCCAATGCCATCATCAGAGATTCTATAACTCAATAGTGAATGTTGCCCAAAACGTGAG 576

QY 161 LeuGlyGluAlaLeuTyrLeuGlyTrpThrThrAlaLeuValLeuIleValGlyGlyAla 180
Db 577 CTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGCTGATTGTTGGAGGAGCT 636

QY 181 LeuPheCysCysValPheCysAsnGluLysSerSerTyrArgTyrSerIlePro 200
Db 637 CTGTTCTGCTGCGTTTTTTTGTGCAACGAAAGAGCAGTAGCTACAGATACTCGATACCT 696

QY 201 SerHisArgThrThrGlnLysSerTyrHisThrGlyLysSerProSerValTyrSer 220
Db 697 TCCCATCGCACAAACCCAAAAAGTTATCACACCGAAAGAAAGTCAACCGAGCGTCTACTCC 756

QY 221 ArgSerGlnTyrVal 225
Db 757 AGAAGTCAGTATGTG 771

RESULT 5

US-10-015-395A-327

; Sequence 327, Application US/10015395A

; Publication No. US20040073015A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan I.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2830P1C57
 ; CURRENT APPLICATION NUMBER: US/10/015,395A
 ; CURRENT FILING DATE: 2001-12-12
 ; Prior application removed - See file Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 477
 ; SEQ ID NO 327
 ; LENGTH: 2010
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
US-10-015-395A-327

Alignment Scores:

Pred. No.: 1.54e-149 Length: 2010
Score: 1172.00 Matches: 225
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-063-732-120 (1-225) x US-10-015-395A-327 (1-2010)

QY 1 MetAlaThrHisAlaLeuGluLeuAlaGlyLeuPheLeuGlyValGlyMetValGly 20
Db 97 ATGGCAACCCATGCCTTAGAAATCGCTGGGCTGTTTCTTGGTGGTGTGAATGGTGGGC 156

QY 21 ThrValAlaValThrValMetProGlnTrpArgValSerAlaPheIleGluAsnAsnIle 40
Db 157 ACAGTGGCTGTCACTGTCAATGCCCTCAGTGGAGAGTGTGGCCCTTCATTGAAACAACATC 216

QY 41 ValValPheGluAsnPheTrpGluGlyLeuTrpMetAsnCysValArgGlnAlaAsnIle 60
Db 217 GTGGTTTTTGAAAACTTCTGGGAAGGACTGTGGATGAATTGGTGAGGCAGGCTAACATC 276

QY 61 ArgMetGlnCysLysIleTyrAspSerLeuLeuAlaLeuSerProAspLeuGlnAlaAla 80
Db 277 AGGATGCAGTGCAAAATCTATGATTCCTGCTGGCTCTTCTCCGACCTACAGGCAGCC 336

QY 81 ArgGlyLeuMetCysAlaAlaSerValMetSerPheLeuAlaPheMetMetAlaIleLeu 100
Db 337 AGAGGACTGATGTGTGCTTCCGTGATGTCCTTCTTGGCTTCATGATGGCCATCCTT 396

QY 101 GlyMetLysCysThrArgCysThrGlyAspAsnGluLysValLysAlaHisIleLeuLeu 120
Db 397 GGCAATGAATGCACCAGGTGCACGGGGACAATGAGAAGGTAAGGCTCACATTCTGCTG 456

QY 121 ThrAlaGlyIleIlePheIleThrGlyMetValValLeuIleProValSerTrpVal 140
Db 457 ACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGTCTCATCCCTGTGAGCTGGGTT 516

QY 141 AlaAsnAlaIleIleArgAspPheTyrAsnSerIleValAsnValAlaGlnLysArgGlu 160
Db 517 GCCAATGCCATCATCAGAGATTCTATAACTCAATAGTGAATGTTGCCCAAAACGTGAG 576

QY 161 LeuGlyGluAlaLeuTyrLeuGlyTrpThrThrAlaLeuValLeuIleValGlyGlyAla 180
Db 577 CTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGCTGATTGTTGGAGGAGCT 636

QY 181 LeuPheCysCysValPheCysAsnGluLysSerSerTyrArgTyrSerIlePro 200
Db 637 CTGTTCTGCTGCGTTTTTTTGTGCAACGAAAGAGCAGTAGCTACAGATACTCGATACCT 696

QY 201 SerHisArgThrThrGlnLysSerTyrHisThrGlyLysSerProSerValTyrSer 220
Db 697 TCCCATCGCACAAACCCAAAAAGTTATCACACCGAAAGAAAGTCAACCGAGCGTCTACTCC 756

; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 357
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-199-670-357

Alignment Scores:
Pred. No.: 1.54e-149 Length: 2010
Score: 1172.00 Matches: 225
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-063-732-120 (1-225) x US-10-199-670-357 (1-2010)

Qy 1 MetAlaThrHisAlaLeuGluIleAlaGlyLeuPheLeuGlyValGlyMetValGly 20
Db 97 ATGGCAACCCATGCCTTAGAAATCGCTGGGCTGTTTCTTTGGTGTGTTGGAATGGTGGC 156
Qy 21 ThrValAlaValThrValMetProGlnTrpArgValSerAlaPheIleGluAsnAsnIle 40
Db 157 ACAGTGGCTGTCACTGTCTATGCCTCAGTGGAGAGTGTCCGCTTCATTGAAAACAACATC 216
Qy 41 ValValPheGluAsnPheTrpGluGlyLeuTrpMetAsnCysValArgGlnAlaAsnIle 60
Db 217 GTGGTTTTTGAAAACCTTCTGGGAAGGACTGTGGATGAATTCGCTGAGGCAGGCTAACATC 276
Qy 61 ArgMetGlnCysLysIleTyrAspSerLeuLeuAlaLeuSerProAspLeuGlnAlaAla 80
Db 277 AGGATGCAGTGCAAAATCTATGATTCCTGCTGGCTCTTTCTCCGGACCTACAGCAGCC 336
Qy 81 ArgGlyLeuMetCysAlaAlaSerValMetSerPheLeuAlaPheMetMetAlaIleLeu 100
Db 337 AGAGGACTGATGTGTGCTGCTCCGTGATGTCTTCTTGGCTTTCATGATGGCCATCCTT 396
Qy 101 GlyMetLysCysThrArgCysThrGlyAspAsnGluLysValLysAlaHisIleLeuLeu 120
Db 397 GGCAATGAATGCACCAAGTGCACGGGGACAAATGAGAAGGTGAAGGCTCACATTCTGCTG 456
Qy 121 ThrAlaGlyIleIlePheIleIleThrGlyMetValValLeuIleProValSerTrpVal 140
Db 457 ACGGCTGGAATCATCTTTCATCATCACGGGCATGGTGGTGTCTCATCCCTGTGAGCTGGTT 516
Qy 141 AlaAsnAlaIleIleArgAspPheTyrAsnSerIleValAsnValAlaGlnLysArgGlu 160
Db 517 GCCAATGCCATCATCAGAGATTCTATAACTCAATAGTGAATGTTGCCCAAAAACGTGAG 576
Qy 161 LeuGlyGluAlaLeuTyrLeuGlyTrpThrAlaLeuValLeuIleValGlyGlyAla 180
Db 577 CTGGAGAAGCTCTCTACTTAGGATGGACCCACGGCACTGGTGTGATTGTTGGAGGAGCT 636
Qy 181 LeuPheCysCysValPheCysCysAsnGluLysSerSerSerTyrArgTyrSerIlePro 200
Db 637 CTGTCTGTGCTGCGTTTTTTTGTGCAACGAAAGACAGTAGCTACAGATACTCGATACCT 696
Qy 201 SerHisArgThrThrGlnLysSerTyrHisThrGlyLysLysSerProSerValTyrSer 220
Db 697 TCCCATGCACAAACCCAAAAGTTATCACACCGAAAGAAAGTATCACACCGAAAGAAAGTATCACCGAGCGTCTACTCC 756
Qy 221 ArgSerGlnTyrVal 225
Db 757 AGAAGTCAGTATGTG 771

RESULT 8

US-10-201-858-357
; Sequence 357, Application US/10201858
; Publication No. US20040038337A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430RIC464
; CURRENT APPLICATION NUMBER: US/10/201,858
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 357
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-201-858-357

Alignment Scores:
Pred. No.: 1.54e-149 Length: 2010
Score: 1172.00 Matches: 225
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-063-732-120 (1-225) x US-10-201-858-357 (1-2010)

Qy 1 MetAlaThrHisAlaLeuGluIleAlaGlyLeuPheLeuGlyValGlyMetValGly 20
Db 97 ATGGCAACCCATGCCTTAGAAATCGCTGGGCTGTTTCTTTGGTGTGTTGGAATGGTGGC 156
Qy 21 ThrValAlaValThrValMetProGlnTrpArgValSerAlaPheIleGluAsnAsnIle 40
Db 157 ACAGTGGCTGTCACTGTCTATGCCTCAGTGGAGAGTGTCCGCTTCATTGAAAACAACATC 216
Qy 41 ValValPheGluAsnPheTrpGluGlyLeuTrpMetAsnCysValArgGlnAlaAsnIle 60
Db 217 GTGGTTTTTGAAAACCTTCTGGGAAGGACTGTGGATGAATTCGCTGAGGCAGGCTAACATC 276
Qy 61 ArgMetGlnCysLysIleTyrAspSerLeuLeuAlaLeuSerProAspLeuGlnAlaAla 80
Db 277 AGGATGCAGTGCAAAATCTATGATTCCTGCTGGCTCTTTCTCCGACCTACAGGCAGCC 336

QY 81 ArgGlyLeuMetCysAlaAlaSerValMetSerPheLeuAlaPheMetMetAlaIleLeu 100
Db 337 AGAGGACTGATGTGTGCTGCTCCGTGATGCTCTTGGCTTTCATGATGGCCATCCTT 396
QY 101 GlyMetLysCysThrArgCysThrGlyAspAsnGluLysValLysAlaHisIleLeuLeu 120
Db 397 GGCATGAAATGCACAGGTGCACGGGGGACATGAGAGGTGAAGGCTCACATTCTGCTG 456
QY 121 ThrAlaGlyIleIlePheIleThrGlyMetValValLeuIleProValSerTrpVal 140
Db 457 ACGGCTGGAATCATCTTTCATCATCACGGGCATGCTGCTGCTCATCCCTGTGAGCTGGTT 516
QY 141 AlaAsnAlaIleIleArgAspPheTyrAsnSerIleValAsnValAlaGlnLysArgGlu 160
Db 517 GCCATGCCATCATCAGAGATTCTATACTCAATAGTGAATGTTGCCCAAAACGTGAG 576
QY 161 LeuGlyGluAlaLeuTyrLeuGlyTrpThrThrAlaLeuValLeuIleValGlyGlyAla 180
Db 577 CTTGGAGAAGCTCTCTACTTAGGATGGACCGCACTGGTGTGCTGATGTTGGAGGAGCT 636
QY 181 LeuPheCysCysValPheCysAsnGluLysSerSerTyrArgTyrSerIlePro 200
Db 637 CTGTTCTGCTGCTGCTTTTGTGCAACGAAAGAGCAGTACAGATACCTCGATACCT 696
QY 201 SerHisArgThrThrGlnLysSerTyrHisThrGlyLysLysSerProSerValTyrSer 220
Db 697 TCCCATCGCACAAACCCAAAAGTTATACACCGGAAAGAGTCAACCGAGCGTCTACTCC 756
QY 221 ArgSerGlnTyrVal 225
Db 757 AGAAGTCAGTATGTG 771

RESULT 9

US-10-205-890-357
; Sequence 357, Application US/10205890
; Publication No. US20040048334A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C519
; CURRENT APPLICATION NUMBER: US/10/205,890
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544

; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 357
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-205-890-357

Alignment Scores: 1.54e-149 Length: 2010
Pred. No.: 1172.00 Matches: 225
Score: 1172.00 Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 13

US-10-063-732-120 (1-225) x US-10-205-890-357 (1-2010)

QY 1 MetAlaThrHisAlaLeuGluIleAlaGlyLeuPheLeuGlyGlyValGlyMetValGly 20
Db 97 ATGGCAACCCATGCCCTTAGAAATCGCTGGCTGTTCTTGGTGGTGTGGAATGGTGGC 156
QY 21 ThrValAlaValThrValMetProGlnTrpArgValSerAlaPheIleGluAsnAsnIle 40
Db 157 ACAGTGGCTGTCACTGTTCATGCCCTCAGTGGAGAGTGTGGCTTTCATTGAAACACATC 216
QY 41 ValValPheGluAsnPheTrpGluGlyLeuTrpMetAsnCysValArgGlnAlaAsnIle 60
Db 217 GTGGTTTTTGAAACTTCTGGGAGGACTGTGGATGAATTCGTGAGGCGAGGTAACATC 276
QY 61 ArgMetGlnCysLysIleTyrAspSerLeuLeuAlaLeuSerProAspLeuGlnAlaAla 80
Db 277 AGGATGCAGTGCAAAATCTATGATTCCTGCTGGCTCTTCTCCGACCTACAGGCAGCC 336
QY 81 ArgGlyLeuMetCysAlaAlaSerValMetSerPheLeuAlaPheMetMetAlaIleLeu 100
Db 337 AGAGGACTGATGTGTGCTGCTTCCGTGATGCTCTTCTTGGCTTTCATGATGGCCATCCT 396
QY 101 GlyMetLysCysThrArgCysThrGlyAspAsnGluLysValLysAlaHisIleLeuLeu 120
Db 397 GGCATGAAATGCACAGGTGCACGGGGGACATGAGAGGTGAAGGCTCACATTCTGCTG 456
QY 121 ThrAlaGlyIleIlePheIleIleThrGlyMetValValLeuIleProValSerTrpVal 140
Db 457 ACGGCTGGAATCATCTTTCATCATCACGGGCATGCTGCTCATCCCTGTGAGCTGGTT 516
QY 141 AlaAsnAlaIleIleArgAspPheTyrAsnSerIleValAsnValAlaGlnLysArgGlu 160
Db 517 GCCATGCCATCATCAGAGATTCTATACTCAATAGTGAATGTTGCCCAAAACGTGAG 576
QY 161 LeuGlyGluAlaLeuTyrLeuGlyTrpThrThrAlaLeuValLeuIleValGlyGlyAla 180
Db 577 CTTGGAGAAGCTCTCTACTTAGGATGGACCGCACCTGGTGTGCTGATGTTGGAGGAGCT 636
QY 181 LeuPheCysCysValPheCysCysAsnGluLysSerSerTyrArgTyrSerIlePro 200
Db 637 CTGTTCTGCTGCTGCTTTTGTGCAACGAAAGAGTCAACCGGAAAGAGTCAACCGAGCGTCTACTCC 756
QY 201 SerHisArgThrThrGlnLysSerTyrHisThrGlyLysLysSerProSerValTyrSer 220
Db 697 TCCCATCGCACAAACCCAAAAGTTATACACCGGAAAGAGTCAACCGGAAAGAGTCAACCGAGCGTCTACTCC 756
QY 221 ArgSerGlnTyrVal 225
Db 757 AGAAGTCAGTATGTG 771

RESULT 10

US-10-208-024-357
; Sequence 357, Application US/10208024
; Publication No. US20040048335A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C538
; CURRENT APPLICATION NUMBER: US/10/208,024
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 357
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-208-024-357

Alignment Scores:
Pred. No.: 1.54e-149 Length: 2010
Score: 1172.00 Matches: 225
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-063-732-120 (1-225) x US-10-208-024-357 (1-2010)

QY 1 MetAlaThrHisAlaLeuGluIleAlaGlyLeuPheLeuGlyGlyValGlyMetValGly 20
Db 97 ATGGCAACCCATGCCTTAGAAATCGCTGGCTGTTTCTTGGTGGTGTGGAAATGGTGGC 156

QY 21 ThrValAlaValThrValMetProGlnTrpArgValSerAlaPheIleGluAsnIle 40
Db 157 ACAGTGGCTGTCACTGTCACTGCTCAGTGGAGAGTGTGGCTTCAATGAAACAACATC 216

QY 41 ValValPheGluAsnPheTrpGluGlyLeuTrpMetAsnCysValArgGlnAlaAsnIle 60
Db 217 GTGGTTTGTGAAACTTCTGGGAAGGACTGTGGATGATTCGTCGAGGCAGCTAACATC 276

QY 61 ArgMetGlnCysLysIleTyrAspSerLeuLeuAlaLeuSerProAspLeuGlnAlaA 80
Db 277 AGGATGCAGTGCAAAATCTATGATCCCTGCTGGCTCTTCTCCGACCTACAGGCAGCC 336

QY 81 ArgGlyLeuMetCysAlaAlaSerValMetSerPheLeuAlaPheMetMetAlaIleLeu 100
Db 337 AGAGGACTGATGTGTGCTGCTCCGTGATGTCCTTCTTGGCTTTCATGATGGCCATCCTT 396

QY 101 GlyMetLysCysThrArgCysThrGlyAspAsnGluLysValLysAlaHisIleLeuLeu 120
Db 397 GGCAATGAAATGCACCAAGGTGCACGGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTG 456

QY 121 ThrAlaGlyIleIlePheIleIleThrGlyMetValValLeuIleProValSerTrpVal 140
Db 457 ACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGCTCATCCCTGTGAGCTGGGTT 516

QY 141 AlaAsnAlaIleIleArgAspPheTyrAsnSerIleValAsnValAlaGlnLysArgGlu 160
Db 517 GCCAATGCCATCATCAGAGATTTCTATAACTCAATAGTAGTAATGTTGCCCAAAACGTGAG 576

QY 161 LeuGlyGluAlaLeuTyrLeuGlyTrpThrThrAlaLeuValLeuIleValGlyGlyAla 180
Db 577 CTTGGAGAAGCTCTCTACTTAGGATGGACCAACGGCACTGGTGCTGATTGTTGGAGGAGCT 636

QY 181 LeuPheCysCysValPheCysCysAsnGluLysSerSerSerTyrArgTyrSerIlePro 200
Db 637 CTGTTCTGCTGCGTTTTTTTGTGCAACGAAAGAGCAGTAGCTACAGATACTCGATACCT 696

QY 201 SerHisArgThrThrGlnLysSerTyrHisThrGlyLysLysSerProSerValTyrSer 220
Db 697 TCCCATCGCACAAACCCAAAAGTTATCACACCGGAAAGAAAGTACAGTACAGATACTACTCC 756

QY 221 ArgSerGlnTyrVal 225
Db 757 AGAAGTCAGTATGTG 771

RESULT 11
US-10-201-853-357
; Sequence 357, Application US/10201853
; Publication No. US20040053358A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C465
; CURRENT APPLICATION NUMBER: US/10/201,853
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 357
; LENGTH: 2010


```
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-201-853-357

Alignment Scores:
Pred. No.: 1.54e-149 Length: 2010
Score: 1172.00 Matches: 225
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-063-732-120 (1-225) x US-10-201-853-357 (1-2010)

QY 1 MetAlaThrHisAlaLeuGluLeuAlaGlyLeuPheLeuGlyGlyValGlyMetValGly 20
Db 97 ATGGCAACCCATGCCCTTAGAAATCGCTGGCTGTTTCTTGGTGGTGTGGAAATGGTGGGC 156

QY 21 ThrValAlaValThrValMetProGlnTrpArgValSerAlaPheIleGluAsnAsnIle 40
Db 157 ACAGTGGCTGTCACTGTATGCCTCAGTGGAGAGTGTGGCTTTCATTGAAACAACATC 216

QY 41 ValValPheGluAsnPheTyrGlyLeuTyrMetAsnCysValArgGlnAlaAsnIle 60
Db 217 GTGGTATGAACTTCTGGGAAGGACTGTGGATGAATTCGTGGCTTTCATGATGGCCATCCT 276

QY 61 ArgMetGlnCysLysIleTyrAspSerLeuAlaLeuSerProAspLeuGlnAlaAla 80
Db 277 AGGATGCAGTGCAAAATCTATGATTCCTGCTGGCTTCTCCGGACCTACAGGCAGCC 336

QY 81 ArgGlyLeuMetCysAlaAlaSerValMetSerPheLeuAlaPheMetMetAlaIleLeu 100
Db 337 AGAGGACTGATGTGTGCTGCTCCGTGATGTCCTTCTTGGCTTTCATGATGGCCATCCT 396

QY 101 GlyMetLysCysThrArgCysThrGlyAspAsnGluLysValLysAlaHisIleLeuLeu 120
Db 397 GGCATGAAATGCACACAGGTGCACGGGGACAATGAGAAAGTGAAAGGCTCACATTCGCTG 456

QY 121 ThrAlaGlyIleIlePheIleIleThrGlyMetValValLeuIleProValSerTrpVal 140
Db 457 ACGGCTGGAATCATCTTCACTTAGGATGGACACGGCACTGGTGTGATTTGGAGGAGCT 516

QY 141 AlaAsnAlaIleIleArgAspPheTyrAsnSerIleValAsnValAlaGlnLysArgGlu 160
Db 517 GCCAATGCCATCATCAGAGATTTCTATAACTCAATAGTAGTGAATGTGCCCCAAAACGTGAG 576

QY 161 LeuGlyGluAlaLeuTyrLeuGlyTyrThrAlaLeuValLeuIleValGlyGlyAla 180
Db 577 CTTGGAGAAGCTCTTACTTAGGATGGACACGGCACTGGTGTGATTTGGAGGAGCT 636

QY 181 LeuPheCysCysValPheCysAsnGluLysSerSerSerTyrArgTyrSerIlePro 200
Db 637 CTGTTCTGCTGCGTTTCTTGTGCAACGAAAGAGCAGTAGCTACAGATACCTCGATACCT 696

QY 201 SerHisArgThrThrGlnLysSerTyrHisThrGlyLysLysSerProSerValTyrSer 220
Db 697 TCCCATCGCACAAACCCAAAAAAGTTATCACACCGGAAAGAGTCAACCGAGCGTCTACTCC 756

QY 221 ArgSerGlnTyrVal 225
Db 757 AGAAGTCAGTATGTG 771
```

```
RESULT 12
US-10-063-745-119
; Sequence 119, Application US/10063745
; Publication No. US20040058411A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
```

```
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,745
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 119
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-745-119

Alignment Scores:
Pred. No.: 1.54e-149 Length: 2010
Score: 1172.00 Matches: 225
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-063-732-120 (1-225) x US-10-063-745-119 (1-2010)

QY 1 MetAlaThrHisAlaLeuGluLeuAlaGlyLeuPheLeuGlyGlyValGlyMetValGly 20
Db 97 ATGGCAACCCATGCCCTTAGAAATCGCTGGCTGTTTCTTGGTGGTGTGGAAATGGTGGGC 156

QY 21 ThrValAlaValThrValMetProGlnTrpArgValSerAlaPheIleGluAsnAsnIle 40
Db 157 ACAGTGGCTGTCACTGTATGCCTCAGTGGAGAGTGTGGCTTTCATTGAAACAACATC 216

QY 41 ValValPheGluAsnPheTyrGlyLeuTyrMetAsnCysValArgGlnAlaAsnIle 60
Db 217 GTGGTATGAACTTCTGGGAAGGACTGTGGATGAATTCGTGGCTTTCATGATGGCCATCCT 276

QY 61 ArgMetGlnCysLysIleTyrAspSerLeuAlaLeuSerProAspLeuGlnAlaAla 80
Db 277 AGGATGCAGTGCAAAATCTATGATTCCTGCTGGCTTCTCCGGACCTACAGGCAGCC 336

QY 81 ArgGlyLeuMetCysAlaAlaSerValMetSerPheLeuAlaPheMetMetAlaIleLeu 100
Db 337 AGAGGACTGATGTGTGCTGCTCCGTGATGTCCTTCTTGGCTTTCATGATGGCCATCCT 396

QY 101 GlyMetLysCysThrArgCysThrGlyAspAsnGluLysValLysAlaHisIleLeuLeu 120
Db 397 GGCATGAAATGCACACAGGTGCACGGGGACAATGAGAAAGTGAAAGGCTCACATTCGCTG 456

QY 121 ThrAlaGlyIleIlePheIleIleThrGlyMetValValLeuIleProValSerTrpVal 140
Db 457 ACGGCTGGAATCATCTTCACTTAGGATGGACACGGCACTGGTGTGATTTGGAGGAGCT 516

QY 141 AlaAsnAlaIleIleArgAspPheTyrAsnSerIleValAsnValAlaGlnLysArgGlu 160
Db 517 GCCAATGCCATCATCAGAGATTTCTATAACTCAATAGTAGTGAATGTGCCCCAAAACGTGAG 576

QY 161 LeuGlyGluAlaLeuTyrLeuGlyTyrThrAlaLeuValLeuIleValGlyGlyAla 180
Db 577 CTTGGAGAAGCTCTTACTTAGGATGGACACGGCACTGGTGTGATTTGGAGGAGCT 636

QY 181 LeuPheCysCysValPheCysAsnGluLysSerSerSerTyrArgTyrSerIlePro 200
Db 637 CTGTTCTGCTGCGTTTCTTGTGCAACGAAAGAGCAGTAGCTACAGATACCTCGATACCT 696

QY 201 SerHisArgThrThrGlnLysSerTyrHisThrGlyLysLysSerProSerValTyrSer 220
Db 697 TCCCATCGCACAAACCCAAAAAAGTTATCACACCGGAAAGAGTCAACCGAGCGTCTACTCC 756

QY 221 ArgSerGlnTyrVal 225
Db 757 AGAAGTCAGTATGTG 771
```

```
RESULT 13
US-10-063-512-119
; Sequence 119, Application US/10063512
; Publication No. US20030018183A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,512
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 119
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-512-119

Alignment Scores:
Pred. No.:      1.54e-149      Length:      2010
Score:          1172.00      Matches:      225
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     100.00%      Indels:      0
DB:              13          Gaps:          0

US-10-063-732-120 (1-225) x US-10-063-512-119 (1-2010)

QY      1  MetAlaThrHisAlaLeuGluIleAlaGlyLeuPheLeuGlyValGlyMetValGly 20
Db      97  ATGGCAACCCATGCCCTTAGAAATCGCTGGGCTGTTTCTTGGTGGTGTGGAATGGTGGC 156
QY      21  ThrValAlaValThrValMetProGlnTrpArgValSerAlaPheIleGluAsnIle 40
Db      157 ACAGTGGCTGTCACTGTATGATCCCTGCTGGCTCTTTCTCCGGACCTACAGCAGCC 216
QY      41  ValValPheGluAsnPheTrpGluGlyLeuTrpMetAsnCysValArgGlnAlaAsnIle 60
Db      217 GTGGTTTTTGAAGAACTTCTGGGAAGGACTGTGGATGAATTGGCTGAGGCAGGTAACATC 276
QY      61  ArgMetGlnCysLysIleTyrAspSerLeuAlaLeuSerProAspLeuGlnAlaAla 80
Db      277 AGGATGCACTGCAAAATCTATGATCCCTGCTGGCTCTTTCTCCGGACCTACAGCAGCC 336
QY      81  ArgGlyLeuMetCysAlaAlaSerValMetSerPheLeuAlaPheMetMetAlaIleLeu 100
Db      337 AGAGGACTGATGTGTGCTTCCGTGATGTCCTTCTTGGCTTTTCATGATGGCCATCCTT 396
QY      101 GlyMetLysCysThrArgCysThrGlyAspAsnGluLysValLysAlaHisIleLeuLeu 120
Db      397 GGCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGTATGTTGCCCAAAACGTGAG 576
QY      141 AlaAsnAlaIleIleArgAspPheTyrAsnSerIleValAsnValAlaGlnLysArgGlu 160
Db      517 GCCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGTATGTTGCCCAAAACGTGAG 576
QY      161 LeuGlyGluAlaLeuTyrLeuGlyTrpThrAlaLeuValLeuIleValGlyGlyAla 180
Db      577 CTTGGAGAAGCTCTCTACTTAGGATGGACCAACGGCACTGGTGTGCTGATTGTTGGAGGAGCT 636
```

```
QY      181 LeuPheCysCysValPheCysCysAsnGluLysSerSerSerTyrArgTyrSerIlePro 200
Db      637 CTGTTCTGCTGCGTTTTTTGTGCAACGAAAGAGCAGTAGCTACAGATACTCGATACCT 696
QY      201 SerHisArgThrThrGlnLysSerTyrHisThrGlyLysLysSerProSerValTyrSer 220
Db      697 TCCCATCGCACAAACCCAAAAAGTTATCACACCGGAAAGAGTACCGAGCGTCTACTCC 756
QY      221 ArgSerGlnTyrVal 225
Db      757 AGAAGTCAGTATGTG 771

RESULT 14
US-10-063-513-119
; Sequence 119, Application US/10063513
; Publication No. US20030018172A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,513
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 119
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-513-119

Alignment Scores:
Pred. No.:      1.54e-149      Length:      2010
Score:          1172.00      Matches:      225
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     100.00%      Indels:      0
DB:              13          Gaps:          0

US-10-063-732-120 (1-225) x US-10-063-513-119 (1-2010)

QY      1  MetAlaThrHisAlaLeuGluIleAlaGlyLeuPheLeuGlyValGlyMetValGly 20
Db      97  ATGGCAACCCATGCCCTTAGAAATCGCTGGGCTGTTTCTTGGTGGTGTGGAATGGTGGC 156
QY      21  ThrValAlaValThrValMetProGlnTrpArgValSerAlaPheIleGluAsnIle 40
Db      157 ACAGTGGCTGTCACTGTATGATCCCTCAGTGGAGAGTGTGGGCTTCATTGAAACACATC 216
QY      41  ValValPheGluAsnPheTrpGluGlyLeuTrpMetAsnCysValArgGlnAlaAsnIle 60
Db      217 GTGGTTTTTGAAGAACTTCTGGGAAGGACTGTGGATGAATTGGCTGAGGCAGGTAACATC 276
QY      61  ArgMetGlnCysLysIleTyrAspSerLeuAlaLeuSerProAspLeuGlnAlaAla 80
Db      277 AGGATGCACTGCAAAATCTATGATCCCTGCTGGCTCTTTCTCCGGACCTACAGCAGCC 336
QY      81  ArgGlyLeuMetCysAlaAlaSerValMetSerPheLeuAlaPheMetMetAlaIleLeu 100
Db      337 AGAGGACTGATGTGTGCTTCCGTGATGTCCTTCTTGGCTTTTCATGATGGCCATCCTT 396
QY      101 GlyMetLysCysThrArgCysThrGlyAspAsnGluLysValLysAlaHisIleLeuLeu 120
Db      397 GGCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGTATGTTGCCCAAAACGTGAG 456
```

QY	121	ThrAlaGlyIleIlePheIleIleThrGlyMetValValLeuIleProValSerTrpVal	140
DB	457	ACGGCTGAATCATCTTCATCATCACGGGCATGGTGGTGCTCATCCCTGTGAGCTGGGTT	516
QY	141	AlaAsnAlaIleIleArgAspPheTyrAsnSerIleValAsnValAlaGlnLysArgGlu	160
DB	517	GCCAAATGCCATCATCAGAGATTCTATAACTCAATAGTGAATGTTGCCCAAAACGTGAG	576
QY	161	LeuGlyGluAlaLeuTyrLeuGlyTrpThrThrAlaLeuValLeuIleValGlyGlyAla	180
DB	577	CTTGGAGAGCTCTCTACTTAGGATGGACCACGGCACTGGTGCTGATTGTTGGAGGAGCT	636
QY	181	LeuPheCysCysValPheCysCysAsnGluLysSerSerTyrArgTyrSerIlePro	200
DB	637	CTGTTCTGCTGCGTTTTTTGTTGTCACACGAAAGAGCAGTAGCTACAGATACTCGATACT	696
QY	201	SerHisArgThrThrGlnLysSerTyrHisThrGlyLysSerProSerValTyrSer	220
DB	697	TCCCATCGCAACACCCAAAAAGTTATCACACCGGAAAGAGTACCGAGCGTCTACTCC	756
QY	221	ArgSerGlnTyrVal	225
DB	757	AGRAGTCAGATGTG	771

RESULT 15
US-10-063-549-119
; Sequence 119, Application US/10063549
; Publication No. US20030027986A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,549
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 119
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-549-119

Alignment Scores:		
Pred. No.:	1.54e-149	Length: 2010
Score:	1172.00	Matches: 225
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	13	Gaps: 0

US-10-063-732-120 (1-225) x US-10-063-549-119 (1-2010)

Qy	1	MetAlaThrHisAlaLeuGluIleAlaGlyLeuPheLeuGlyGlyValGlyMetValGly	20
Db	97	ATGGCAACCCATGCCTTAGAAATCGCTGGSGCTTTCTTGGTGGTGTGGAAATGGTGGC	156
Qy	21	ThrValAlaValThrValMetProGlnTrpArgValSerAlaPheIleGluAsnAsnIle	40
Db	157	ACAGTGGCTGTCACTGTCAATGCCTCAGTGAGAGAGTGTCGGCCTTCATTGAAAAACAACATC	216
Qy	41	ValValPheGluAsnPheTrpGluGlyLeuTrpMetAsnCysValArgGlnAlaAsnIle	60
Db	217	GTGGTTTTTGAAAACTTCTGGGAAGGACTGTGGATGAATTGCGTGAGCGAGGCTTAACATC	276

QY	61	ArgMetGlnCysLysIleTyrAspSerLeuAlaLeuSerPheLeuAlaLeuSerProAspLeuGlnAlaAla	80
DB	277	AGGATGCAGTGCAAAATCTATGATCCCTGCTGGCTCTTTCTCGGACCTACAGGCAGCC	336
QY	81	ArgGlyLeuMetCysAlaAlaSerValMetSerPheLeuAlaPheMetMetAlaIleLeu	100
DB	337	AGAGACTGATGTGTGCTGCTTCGGTGATGTCTTCTTGGCTTTCATGATGGCCATCCTT	396
QY	101	GlyMetLysCysThrArgCysThrGlyAspAsnGluLysValLysAlaHisIleLeuLeu	120
DB	397	GGCATGAATGCACCAGGTGCACGGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTG	456
QY	121	ThrAlaGlyIleIlePheIleIleThrGlyMetValValLeulleProValSerTrpVal	140
DB	457	ACGGCTGGAATCATCTTTCATCATCACGGGCATGGTGGTGCTCATCCCTGTGAGCTGGGTT	516
QY	141	AlaAsnAlaIleIleArgAspPheTyrAsnSerIleValAsnValAlaGlnLysArgGlu	160
DB	517	GCCAATGCCATCATCAGAGATTCTATAAECTCAATAGTAGTAATGTGCCCAAAAACGTGAG	576
QY	161	LeuGlyGluAlaLeuTyrLeuGlyTrpThrThrAlaLeuValLeulleValGlyGlyAla	180
DB	577	CTTGAGAAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGCTGATTGTTGGAGGAGCT	636
QY	181	LeuPheCysCysValPheCysCysAsnGluLysSerSerSerTyrArgTyrSerIlePro	200
DB	637	CTGTTCTGCTGCGTTTTTTTGTGCAACGAAAGAGCAGTAGCTACAGATACTCGATACT	696
QY	201	SerHisArgThrThrGlnLysSerTyrHisThrGlyLysLysSerProSerValTyrSer	220
DB	697	TCCCATCGCACACCCAAAAAAGTTATCACACCGGAAAGAGTCAACCGAGCGTCTACTCC	756
QY	221	ArgSerGlnTyrVal	225
DB	757	AGAAAGTCAGTATGTG	771

Search completed: September 3, 2004, 04:47:59
Job time : 488 secs

Db	1	MAFYPLQIAGLVLFGLVGTIGTTLLPQWRVSFAFIGSNIIFERIWEGLWMNCIQQAMV	60
QY	61	RMQCKIYDLSLLSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL	120
Db	61	TLQCKFYNSILALPPVLEAARALMCVAVALVALIIGICGMKQLQCTGSSERVKAYLLG	120
QY	121	TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGTWTALVLIVGGA	180
Db	121	TSGVLFILTGIFVLIPVSWTANIIIRDFYDPTVHAGQKRELGGALFLGWATAAVLFIGGG	180
QY	181	LFCCVFCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV	225
Db	181	LLCGYCCCNRKERWHRYPVPAYRVPQKDNQRNVTVPRKSSTS-YV	224
RESULT 2			
Q805G0	PRELIMINARY; PRT; 213 AA.		
AC	Q805G0;		
DT	01-JUN-2003	(TReMBLrel. 24, Created)	
DT	01-JUN-2003	(TReMBLrel. 24, Last sequence update)	
DT	01-OCT-2003	(TReMBLrel. 25, Last annotation update)	
DE	Claudin4L2.		
GN	CLDN4L2.		
OS	Xenopus laevis (African clawed frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;		
OC	Xenopodinae; Xenopus.		
OX	NCBI_TaxID=8355;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Fujita M., Itoh M., Shibata M., Taira S., Taira M.;		
RT	"Gene expression pattern analysis of the tight junction protein,		
RT	Claudin, in the early morphogenesis of Xenopus embryos.";		
RL	Gene Expr. Patterns 2:23-26(2002).		
DR	EMBL; AB072909; BAC21014.1; -.		
DR	GO; GO:0016020; C:membrane; IEA.		
DR	GO; GO:0005923; C:tight junction; IEA.		
DR	GO; GO:0005198; F:structural molecule activity; IEA.		
DR	InterPro; IPR006187; Claudin.		
DR	InterPro; IPR006188; Claudin reg.		
DR	InterPro; IPR004031; PMP22_Claudin.		
DR	Pfam; PF00822; PMP22_Claudin; 1.		
DR	PRINTS; PR01077; CLAUDIN.		
DR	PROSITE; PS01346; CLAUDIN; 1.		
SQ	SEQUENCE 213 AA; 22913 MW; ACF10FC95F9C16A1 CRC64;		
Query Match 45.9%; Score 538; DB 13; Length 213;			
Best Local Similarity 45.8%; Pred. No. 1.3e-45;			
Matches 103; Conservative 43; Mismatches 67; Indels 12; Gaps 4;			
QY	1	MATHALEIAGLFLGGVGMGTAVTVMPQWRVSFAFIENNIIVFENFWGLWMNCVRQANI	60
Db	1	MASTGLQILGMALIGWVGCIITCALPMWRVTAFIGNNIVVAQTIWGLWMNCIVQSTG	60
QY	61	RMQCKIYDLSLLSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL	120
Db	61	QMCKVYDSMLALSQDLQAARALTVCILVALLAMLIGVVGAKCTNCIED-KNAKAKVSM	119
QY	121	TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGTWTALVLIVGGA	180
Db	120	VSGIVFLVAGILLIPVCWSANSIIRDFYNPLVVEAQKRELGAALYIGWASAALMLLGGG	179
QY	181	LFCCVFCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV	225
Db	180	LLCC--SCPREDNH-YS-----AQYTAASQPRSDYPSKNYV	213
RESULT 3			
Q98SR2	PRELIMINARY; PRT; 214 AA.		
ID	Q98SR2		
AC	Q98SR2;		
DT	01-JUN-2001	(TReMBLrel. 17, Created)	

DT	01-JUN-2001	(TrEMBLrel. 17, Last sequence update)	
DT	01-JUN-2003	(TrEMBLrel. 24, Last annotation update)	
DE	Claudin-3.		
GN	CLDN3.		
OS	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
OC	Gallus.		
OX	NCBI_TaxID=9031;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Reardon E., Kojima S., Rizzolo L.J.;		
RT	"Sequence of chick claudin-3 cDNA.";		
RL	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF334677; AAK20876.1; -.		
DR	GO; GO:0016020; C:membrane; IEA.		
DR	GO; GO:0005923; C:tight junction; IEA.		
DR	GO; GO:0005198; F:structural molecule activity; IEA.		
DR	InterPro; IPR006187; Claudin.		
DR	InterPro; IPR006188; Claudin.reg.		
DR	InterPro; IPR004031; PMP22_Claudin.		
DR	Pfam; PF00822; PMP22_Claudin; 1.		
DR	PRINTS; PR01077; CLAUDIN.		
DR	PROSITE; PS01346; CLAUDIN; 1.		
SQ	SEQUENCE 214 AA; 23090 MW; A2540116CBD53978 CRC64;		
Query Match 45.9%; Score 538; DB 13; Length 214;			
Best Local Similarity 48.6%; Pred. No. 1.3e-45;			
Matches 107; Conservative 38; Mismatches 65; Indels 10; Gaps 4;			
Qy	6	LEIAGLFLGGVGMGTAVTVMPQWRVSFAFIENNIIVFENFWGLWMNCVRQANIRMQCK	65
Db	5	LEIGGVALSVLGLWLCIIICCALPMWRVTAFIGNNIVTAQIIWGLWMNCVVQSTGMQCK	64
Qy	66	IYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGII	125
Db	65	VYDSMLALPQDLQAARALLVVAIVLAVLGLMVAIVGAQCTRCVED-ETTKAKITIVSGVI	123
Qy	126	FIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGTWTALVLIVGGALFCCV	185
Db	124	FLLSGIMTLIPVSWSANTIIRDFYNPLVIDAQKRELGTSLYVGWAASALLLFGGALLCC-	182
Qy	186	FCCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV	225
Db	183	-SCPPKDERY---APS----KVAYSAPRSVTSYDKRNVV	214
RESULT 4			
ID	Q90XQ9	PRELIMINARY;	PRT; 214 AA.
AC	Q90XQ9;		
DT	01-DEC-2001	(TrEMBLrel. 19, Created)	
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)	
DT	01-JUN-2003	(TrEMBLrel. 24, Last annotation update)	
DE	Claudin A (Claudin4L1).		
GN	CLDNA OR CLDN4L1.		
OS	Xenopus laevis (African clawed frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;		
OC	Xenopodinae; Xenopus.		
OX	NCBI_TaxID=8355;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21417738; PubMed=11517306;		
RA	Kollmar R., Nakamura S.K., Kappler J.A., Hudspeth A.J.;		
RT	"Expression and phylogeny of claudins in vertebrate primordia.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 98:10196-10201(2001).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Fujita M., Itoh M., Shibata M., Taira S., Taira M.;		
RT	"Gene expression pattern analysis of the tight junction protein,		
RT	Claudin, in the early morphogenesis of Xenopus embryos.";		
RL	Gene Expr. Patterns 2:23-26(2002).		

DR EMBL; AF359435; AAL01842.1; --
DR EMBL; AB072908; BAC21013.1; --
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005923; C:tight junction; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR006188; Claudin reg.
DR InterPro; IPR004031; PMP22 Claudin.
DR Pfam; PF00822; PMP22 Claudin; 1.
DR PRINTS; PR01077; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN; 1.
SQ SEQUENCE 214 AA; 22952 MW; 8E86F0EB2B72357D CRC64;

Query Match 45.9%; Score 538; DB 13; Length 214;
Best Local Similarity 48.5%; Pred. No. 1.3e-45;
Matches 99; Conservative 43; Mismatches 56; Indels 6; Gaps 3;

QY 1 MATHALEIAGLFLGGVGMVGTAVTVMPQWRVSAFIENNVFENFWEGLMNCVRQANI 60
Db 1 MASTGLQVLGMAISIIGWVGCIIITCAMPMWRVTAFIGNNVVAQIIWEGLMNCIVQSTG 60
QY 61 RMQCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120
Db 61 QMCKVYDSMLALPQDLQAARALTVCILVALLAMLVGIVGAKCTNCIED-ENTKAKVSM 119
QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGA 180
Db 120 VSGVFLVAGILMLIPVCWSANSIIRDFYNPLVVEAQKRELGAALYIGWASSALMLLGGG 179
QY 181 LFCCVFCCKNEKSS--SYRSIPS 201
Db 180 LLCC--SCPKNADAPYSARYTAPS 201

RESULT 5
Q9DE12 PRELIMINARY; PRT; 214 AA.
AC Q9DE12;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Transmembrane tight junction protein claudin.
GN CLA.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Dorsal lip;
RX MEDLINE=21098758; PubMed=11161574;
RA Brizuela B.J., Wessely O., De Robertis E.M.;
RT "Overexpression of the Xenopus Tight-Junction Protein Claudin Causes
RL Randomization of the Left-Right Body Axis.";
RL Dev. Biol. 230:217-229(2001).
DR EMBL; AF224712; AAG44257.1; --
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005923; C:tight junction; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR006188; Claudin reg.
DR InterPro; IPR004031; PMP22 Claudin.
DR Pfam; PF00822; PMP22 Claudin; 1.
DR PRINTS; PR01077; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN; 1.
SQ SEQUENCE 214 AA; 23151 MW; 3F0D65E3ADE311E6 CRC64;

Query Match 45.5%; Score 533; DB 13; Length 214;
Best Local Similarity 47.9%; Pred. No. 4e-45;
Matches 103; Conservative 43; Mismatches 61; Indels 8; Gaps 4;

QY 1 MATHALEIAGLFLGGVGMVGTAVTVMPQWRVSAFIENNVFENFWEGLMNCVRQANI 60

Db 1 MASTGLQILGMAMSIIGWVGSIIISCALPMWRVTAFIGNNVVAQIIWEGLMNCIVQSTG 60
QY 61 RMQCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120
Db 61 QMCKVYDSMLALPQDLQAARALTVCILVALLAMFIVGAKCTNCIED-ENTKAKVSM 119
QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGA 180
Db 120 VSGIVFLVAGILMLIPVCWSANSIIRDFYNPLVVEAQKRELGAALYIRWASSAILLLGGS 179
QY 181 LFCCVFCCKNEKSSSY--RYSIPS----HRTTQKSY 209
Db 180 LLCC-SCPKNADAPYPARYTAPSCPPRSPDYTSKNY 213

RESULT 6
Q90XR9 PRELIMINARY; PRT; 209 AA.
AC Q90XR9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Claudin e.
GN CLDNE.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21417738; PubMed=11517306;
RA Kollmar R., Nakamura S.K., Kappler J.A., Hudspeth A.J.;
RT "Expression and phylogeny of claudins in vertebrate primordia.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:10196-10201(2001).
DR EMBL; AF359425; AAL01832.1; --
DR ZFIN; ZDB-GENE-010328-5; cldne.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005923; C:tight junction; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR005411; Claudin2.
DR InterPro; IPR006188; Claudin reg.
DR InterPro; IPR004031; PMP22 Claudin.
DR Pfam; PF00822; PMP22 Claudin; 1.
DR PRINTS; PR01077; CLAUDIN.
DR PRINTS; PR01589; CLAUDIN2.
DR PROSITE; PS01346; CLAUDIN; 1.
SQ SEQUENCE 209 AA; 22593 MW; A86F48D852E16CB2 CRC64;

Query Match 44.7%; Score 523.5; DB 13; Length 209;
Best Local Similarity 47.4%; Pred. No. 3.5e-44;
Matches 100; Conservative 37; Mismatches 69; Indels 5; Gaps 3;

QY 1 MATHALEIAGLFLGGVGMVGTAVTVMPQWRVSAFIENNVFENFWEGLMNCVRQANI 60
Db 1 MVSMCREILGMCLAIIGFLGAIICALPMWKVTAFIGANIVTAQTIWEGLMNCVMQSTG 60
QY 61 RMQCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120
Db 61 QMCKIYDSLALPQDLQAARALVVAIIIVFFALILGIAGKCTNFV-EREDAKAKVSI 119
QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGA 180
Db 120 ASGVIFIIAGVLVLPVCWSANSIIRDFYNPLLTDAQRREMGASLYIGWVAALLIIGG 179
QY 181 LFCCVFCCKNEKSSSY--RYSIPSHRTTQKSY 209
Db 180 ILCS--SCPDKENKYSQPRSTRATSRAY 208

RESULT 7

Db 65 VDSMLALGQDLQASRAMTVIAIILAVLGVMLISVMGAKCTNCIED-EGAKAKMIVSGIM 123

Qy 126 FIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCV 185

Db 124 FIAGILDIPSANVANQIIRDFYNPLPGAQORELGASIIYIGFAAAALLIIGGAMLCCT 183

Qy 186 FCCNEKSSSYRYSIPSHRTTQKSYHTGKKSPPSVYSRSQYV 225

Db 184 --CPPKEKKY-----KPARMGYSAPRSASAGYDKKDYV 214

RESULT 10

Q7T2P4

ID Q7T2P4 PRELIMINARY; PRT; 214 AA.

AC Q7T2P4;

DT 01-OCT-2003 (TReMBLrel. 25, Created)

DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)

DE Claudin h.

OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI_TaxID=7955;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,

RA Blakesley R.W., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RA Strausberg R.;

RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

DR EMBL; BC053223; AAH53223.1; -.

SQ SEQUENCE 214 AA; 22792 MW; D896FD3E50DEF518 CRC64;

Query Match 43.9%; Score 514; DB 13; Length 214;

Best Local Similarity 43.6%; Pred. No. 3.2e-43;

Matches 96; Conservative 46; Mismatches 58; Indels 10; Gaps 3;

QY 6 LEIAGLFLGGVGMGTAVTVMPPQWRVSAFIENNIIVVFENFWEGLWMNCVROANIRMOCK 65

Db 5 LEIGGIALGIIGWIIISIVACALPMWRVSAFVGANIVTAQVMDGLWMNCVQSTGQMCK 64

QY 66 IYDSLIALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGII 125

Db 65 VDSMLALGQDLQASRAMTVIAIILAVLGVMLISVMGAKCTNCIED-EGAKAKMIVSGIM 123

QY 126 FIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCV 185

Db 124 FIAGILDIPSANVANQIIRDFYNPLPGAQORELGASIIYIGFAAAALLIIGGAMLCCT 183

Qy 186 FCCNEKSSSYRYSIPSHRTTQKSYHTGKKSPPSVYSRSQYV 225

Db 184 --CPPKEKKY-----KPARMGYSAPRSASAGYDKKDYV 214

RESULT 11

Q90XR4

ID Q90XR4 PRELIMINARY; PRT; 210 AA.

AC Q90XR4;

DT 01-DEC-2001 (TReMBLrel. 19, Created)

DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)

DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)

DE Claudin j.

GN CLDNJ.

OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI_TaxID=7955;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21417738; PubMed=11517306;

RA Kollmar R., Nakamura S.K., Kappler J.A., Hudspeth A.J.;

RT "Expression and phylogeny of claudins in vertebrate primordia.";

RL Proc. Natl. Acad. Sci. U.S.A. 98:10196-10201 (2001).

DR EMBL; AF359430; AAL01837.1; -.

DR ZFIN; ZDB-GENE-010328-10; cldnj.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0005923; C:tight junction; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR006187; Claudin.

DR InterPro; IPR006188; Claudin_reg.

DR InterPro; IPR004031; PMP22 Claudin.

DR Pfam; PF00822; PMP22 Claudin.

DR PRINTS; PR01077; CLAUDIN.

DR PROSITE; PS01346; CLAUDIN; 1.

SQ SEQUENCE 210 AA; 22895 MW; F9A6964463E55775 CRC64;

Query Match 42.9%; Score 503; DB 13; Length 210;

Best Local Similarity 43.0%; Pred. No. 3.9e-42;

Matches 95; Conservative 47; Mismatches 67; Indels 12; Gaps 4;

QY 5 ALEIAGLFLGGVGMGTAVTVMPPQWRVSAFIENNIIVVFENFWEGLWMNCVROANIRMOCK 64

Db 2 ALQVLGITLSMIGFAGTIIICALPMWKVTAFIGTNIIVVAQVFWEGLTWMTCVVERIGQMOC 61

QY 65 KIYDSLIALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI 124

Db 62 KLYDALLDLPFLQASRGLIVTTMALASLAFILIFIGADCTNCL-SNPRAKGRIVVSGI 120

QY 125 IFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCC 184

Db 121 TFMLSGLTTVPVPSWTADSIIRDHNPVVEALKREMGAAALYVGLTAGFLVVGAILCT 180

QY 185 VFCNEKSSSYRYSIPSHRTTQKSYHTGKKSPPSVYSRSQYV 225

Db 181 --SCPPERDNY---LPRYTLTKSGTHSG-----YAVKNYV 210

RESULT 12

Q90XR2

ID Q90XR2 PRELIMINARY; PRT; 218 AA.

AC Q90XR2;

DT 01-DEC-2001 (TReMBLrel. 19, Created)

DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)

DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)

DE Claudin c.

GN CLDNC.

OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI_TaxID=7955;

RN [1]

Search completed: September 1, 2004, 16:55:38
Job time : 42 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2004, 16:52:38 ; Search time 18 Seconds
(without alignments)
645.325 Million cell updates/sec

Title: US-10-063-732-120
Perfect score: 1172
Sequence: 1 MATHALEIAGLFLGVGMVG.....QKSYHTGKKSPSVYRSQYV 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	534	45.6	220	4	US-09-603-552-13
2	530	45.2	113	4	US-09-621-976-5695
3	489	41.7	247	4	US-09-130-491-15
4	479	40.9	202	4	US-09-205-258-344
5	477.5	40.7	218	4	US-09-130-491-14
6	477.5	40.7	218	4	US-09-489-847-209
7	470	40.1	225	4	US-09-673-395A-354
8	439	37.5	211	4	US-09-130-491-4
9	439	37.5	211	4	US-09-603-552-12
10	439	37.5	211	4	US-09-886-683A-4
11	372.5	31.8	230	4	US-09-663-600A-186
12	363.5	31.0	230	4	US-09-663-600A-92
13	310.5	26.5	264	4	US-09-724-864-64
14	296	25.3	228	4	US-09-603-552-1
15	294	25.1	137	3	US-09-188-930-174
16	294	25.1	137	4	US-09-312-283C-174
17	204	17.4	99	4	US-09-621-976-4220
18	201	17.2	207	1	US-08-557-917A-2
19	201	17.2	207	3	US-09-084-153-2
20	201	17.2	207	3	US-09-084-079-2
21	190	16.2	218	3	US-09-084-079-5
22	143	12.2	72	4	US-09-489-847-366
23	143	12.2	73	4	US-09-489-847-241
24	115	9.8	323	4	US-09-123-030-8
25	108	9.2	32	4	US-09-205-258-872
26	92.5	7.9	831	2	US-08-677-734A-11
27	92.5	7.9	831	4	US-09-097-053-11

28	91.5	7.8	445	4	US-09-328-352-6669	Sequence 6669, Ap
29	87.5	7.5	834	2	US-08-677-734A-9	Sequence 9, Appli
30	87.5	7.5	834	2	US-08-677-734A-10	Sequence 10, Appl
31	87.5	7.5	834	4	US-09-097-053-9	Sequence 9, Appli
32	87.5	7.5	834	4	US-09-097-053-10	Sequence 10, Appl
33	85.5	7.3	832	2	US-08-677-734A-12	Sequence 12, Appl
34	85.5	7.3	832	4	US-09-097-053-12	Sequence 12, Appl
35	85	7.3	157	2	US-08-883-070-3	Sequence 3, Appli
36	83	7.1	548	3	US-08-903-139B-28	Sequence 28, Appl
37	81.5	7.0	315	4	US-09-123-030-10	Sequence 10, Appl
38	81	6.9	159	4	US-09-134-001C-4062	Sequence 4062, Ap
39	81	6.9	327	3	US-09-392-014-2	Sequence 2, Appli
40	80	6.8	223	4	US-09-266-764-2	Sequence 2, Appli
41	80	6.8	327	4	US-09-123-030-12	Sequence 12, Appl
42	79.5	6.8	422	4	US-09-489-039A-7295	Sequence 7295, Ap
43	79.5	6.8	472	4	US-09-934-899-10	Sequence 10, Appl
44	79	6.7	22	4	US-09-205-258-869	Sequence 869, App
45	79	6.7	263	4	US-09-134-000C-5703	Sequence 5703, Ap

ALIGNMENTS

RESULT 1
US-09-603-552-13
; Sequence 13, Application US/09603552
; Patent No. 6590089
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Tang, Y. Tom
; APPLICANT: Patterson, Chandra
; TITLE OF INVENTION: RVP-1 VARIANT DIFFERENTIALLY EXPRESSED IN CROHN'S DISEASE
; FILE REFERENCE: PC-0016 US
; CURRENT APPLICATION NUMBER: US/09/603,552
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank No. 6590089 g2570129
US-09-603-552-13

Query Match	45.6%	Score 534;	DB 4;	Length 220;
Best Local Similarity	46.2%	Pred. No. 9.2e-52;		
Matches 104;	Conservative 35;	Mismatches 72;	Indels 14;	Gaps 4;
QY	6	LEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNIVFENFWEGLMNCVQRQANIRMQCK 65		
Db	5	LEITGTALAVLGLTIVCCALPMWRVSFIGSNIITSONIWEGLMNCVQSTGQMCK 64		
QY	66	IYDSSLALSPDLQARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGII 125		
Db	65	VYDSSLALPQDLQARALIWAIIAALFGLLVALVGAQCTNCVQD-DTAKAKITIVAGVL 123		
QY	126	FIITGMVVLIPVSWVANAIIRDVNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCV 185		
Db	124	FLLAALLTLVPVSWSANTIIRDVFNYPVPEAQKREMGAGLYVGWAAAALQLLGGALLCC- 182		
QY	186	FCCNEKSSSYR-----YSIPSHRTTQKSYHTGKKSPSVYRSQYV 225		
Db	183	-SCPPREKKYTATKVVISAPRSTGPGASLGTG-----YDRKDYV 220		

RESULT 2
US-09-621-976-5695
; Sequence 5695, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 5695
LENGTH: 113
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -79..-1
NAME/KEY: UNSURE
LOCATION: 25
OTHER INFORMATION: Xaa = * ,Ser
US-09-621-976-5695

Query Match 45.2%; Score 530; DB 4; Length 113;
Best Local Similarity 100.0%; Pred. No. 1e-51;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNVVFFENFWEGLMNCVRQANI 60
Db 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNVVFFENFWEGLMNCVRQANI 60
QY 61 RMOCKIYDLSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMK 103
Db 61 RMOCKIYDLSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMK 103

RESULT 3
US-09-130-491-15
Sequence 15, Application US/09130491
Patent No. 6416974
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
FILE REFERENCE: 09404/041001
CURRENT APPLICATION NUMBER: US/09/130,491
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: US 60/058,108
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: US 60/054,961
EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 15
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-09-130-491-15

Query Match 41.7%; Score 489; DB 4; Length 247;
Best Local Similarity 42.6%; Pred. No. 1.2e-46;
Matches 100; Conservative 41; Mismatches 72; Indels 22; Gaps 4;
QY 5 ALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNVVFFENFWEGLMNCVRQANIRMQC 64
Db 4 SLEITGTSIAVLGLWLTIVCCALPMWRVSAFIGSSIIITAQITWEGLMNCV-QSTGQMOC 62
QY 65 KIYDLSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI 124
Db 63 KMYDLSLLALPQDLQARALIVVSILLAAFGLLVALVGAQCTNCVQD-ETAKAKITIVAGV 121
QY 125 IFPIITGMVVLIPVSVWANAIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCC 184
Db 122 LFLAAAVLTLPVPSWSANTIRDFYNPLVPEAQKREMGTLGVGWAAAALQLLGGALLCC 181
QY 185 VFCNEKSSYR--YSIP-----SHRTTQKSYHTGKSPSVY 219

Db 182 SCPPREKYAPTILYSAPRSTGPGTGTGTAYDRKTTSERPGARTPHHHHYQPSMY 236
RESULT 4
US-09-205-258-344
Sequence 344, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974

Db 180 LLCAGWVCTGRPDLSFPVKYSAPRRPTA-----TGD-----YDKKNYV 218

RESULT 7

US-09-673-395A-354

; Sequence 354, Application US/09673395A

; Patent No. 6620923

; GENERAL INFORMATION:

; APPLICANT: SPECHT, THOMAS

; APPLICANT: HINZMANN, BERND

; APPLICANT: SCHMITT, ARMIN

; APPLICANT: PILARSKI, CHRISTIAN

; APPLICANT: DAHL, EDGAR

; APPLICANT: ROSENTHAL, ANDRE

; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE

; FILE REFERENCE: ALBRE-12

; CURRENT APPLICATION NUMBER: US/09/673,395A

; CURRENT FILING DATE: 2000-10-17

; NUMBER OF SEQ ID NOS: 637

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 354

; LENGTH: 225

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-673-395A-354

Query Match 40.1%; Score 470; DB 4; Length 225;

Best Local Similarity 40.9%; Pred. No. 1.4e-44;

Matches 92; Conservative 42; Mismatches 77; Indels 14; Gaps 2;

QY 1 MATHALEIAGLFLGGVGMGTAVTVMPPQWRVSFAFIENNIIVFENFWEGLWMNCVRQANI 60

Db 15 MANSGLQLLGFSSMALLGWVGLVACTAIPQWQMSSYAGDNIITAQAMYKGLWMDCVTQSTG 74

QY 61 RMOCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKTRCTGDNEKVKAHILL 120

Db 75 MMSCKMYDSVLALSAAALQATRALMVVSLVLGFLAMFVATMGKTRCGGDDKVKKARIAM 134

QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIIVGGA 180

Db 135 GGGIIFIVAGLAALVACSWYGHQIVTDFYNPLIPTNIKYEFGFAIFIGWAGSALVILGGA 194

QY 181 LFCCVFCCKEKKSSSYRYSIPSHRTTQKSYHTGKKSPSVYRSQYV 225

Db 195 LLSCSCPGNESKAGYR-----APRSY-----PKSNSKEYV 225

RESULT 8

US-09-130-491-4

; Sequence 4, Application US/09130491

; Patent No. 6416974

; GENERAL INFORMATION:

; APPLICANT: Holtzman, Douglas A.

; APPLICANT: Goodearl, Andrew D.J.

; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83

; FILE REFERENCE: 09404/041001

; CURRENT APPLICATION NUMBER: US/09/130,491

; CURRENT FILING DATE: 1998-08-07

; EARLIER APPLICATION NUMBER: US 60/058,108

; EARLIER FILING DATE: 1997-09-05

; EARLIER APPLICATION NUMBER: US 60/054,961

; EARLIER FILING DATE: 1997-08-06

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 4

; LENGTH: 211

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-130-491-4

Query Match 37.5%; Score 439; DB 4; Length 211;

Best Local Similarity 36.9%; Pred. No. 3.8e-41;

Matches 83; Conservative 48; Mismatches 80; Indels 14; Gaps 3;

QY 1 MATHALEIAGLFLGGVGMGTAVTVMPPQWRVSFAFIENNIIVFENFWEGLWMNCVRQANI 60

Db 1 MANAGLQLLGFILAFILGWIGAIIVSTALPQWRIYSYAGDNIIVTAQAMYEGLWMSCVSQSTG 60

QY 61 RMOCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKTRCTGDNEKVKAHILL 120

Db 61 QIQCKVFDLSLNLSTLQATRALMVVGLILGVIAIFVATVGMKMKCLEDDDEVQKRMVAV 120

QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIIVGGA 180

Db 121 IGGAIFFLLAGLAILVATAWYGNRIVQEFYDPMTPVNARYEFGQALFTGMAAASLCLLGGGA 180

QY 181 LFCCVFCCKEKKSSSYRYSIPSHRTTQKSYHTGKKSPSVYRSQYV 225

Db 181 LLCC--SCPRKTTSY----PTPRYPK-----PAPSSGKDYV 211

RESULT 9

US-09-603-552-12

; Sequence 12, Application US/09603552

; Patent No. 6590089

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Tang, Y. Tom

; APPLICANT: Patterson, Chandra

; TITLE OF INVENTION: RVP-1 VARIANT DIFFERENTIALLY EXPRESSED IN CROHN'S DISEASE

; FILE REFERENCE: PC-0016 US

; CURRENT APPLICATION NUMBER: US/09/603,552

; CURRENT FILING DATE: 2000-06-22

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PERL Program

; SEQ ID NO 12

; LENGTH: 211

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No. 6590089 2057608CD1

US-09-603-552-12

Query Match 37.5%; Score 439; DB 4; Length 211;

Best Local Similarity 36.9%; Pred. No. 3.8e-41;

Matches 83; Conservative 48; Mismatches 80; Indels 14; Gaps 3;

QY 1 MATHALEIAGLFLGGVGMGTAVTVMPPQWRVSFAFIENNIIVFENFWEGLWMNCVRQANI 60

Db 1 MANAGLQLLGFILAFILGWIGAIIVSTALPQWRIYSYAGDNIIVTAQAMYEGLWMSCVSQSTG 60

QY 61 RMOCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKTRCTGDNEKVKAHILL 120

Db 61 QIQCKVFDLSLNLSTLQATRALMVVGLILGVIAIFVATVGMKMKCLEDDDEVQKRMVAV 120

QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIIVGGA 180

Db 121 IGGAIFFLLAGLAILVATAWYGNRIVQEFYDPMTPVNARYEFGQALFTGMAAASLCLLGGGA 180

QY 181 LFCCVFCCKEKKSSSYRYSIPSHRTTQKSYHTGKKSPSVYRSQYV 225

Db 181 LLCC--SCPRKTTSY----PTPRYPK-----PAPSSGKDYV 211

RESULT 10

US-09-886-683A-4

; Sequence 4, Application US/09886683A

; Patent No. 6627439

; GENERAL INFORMATION:

; APPLICANT: Hoevel, Thorsten

; APPLICANT: Koch, Stefan

; APPLICANT: Kubbies, Manfred

; APPLICANT: Mundigl, Olaf

; APPLICANT: Rueger, Petra

; TITLE OF INVENTION: Antibodies against SEMP1 (p23)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2004, 16:53:38 ; Search time 16 Seconds
(without alignments)
1352.693 Million cell updates/sec

Title: US-10-063-732-120
Perfect score: 1172
Sequence: 1 MATHALEIAGLFLGGVMVG.....QKSYHTGKKSPSVYRSQYV 225
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	489	41.7	280	A39484	androgen-withdrawa
2	100.5	8.6	660	A44432	amino acid transpo
3	99.5	8.5	173	A49182	integral membrane
4	97.5	8.3	459	S10196	NADH2 dehydrogenas
5	95.5	8.1	173	A48300	lens membrane prot
6	94.5	8.1	459	T11489	NADH2 dehydrogenas
7	94	8.0	468	T33784	hypothetical prote
8	93	7.9	484	C75609	amino acid ABC tra
9	92.5	7.9	637	S48921	hypothetical prote
10	92.5	7.9	831	B40204	Na+/H+-exchanging
11	91.5	7.8	988	S37078	chloride channel p
12	89.5	7.6	380	AH0781	probable membrane
13	89	7.6	440	T11358	NADH2 dehydrogenas
14	88	7.5	618	S33044	hypothetical prote
15	87	7.4	297	T23909	hypothetical prote
16	87	7.4	664	S59638	glucose transport
17	87	7.4	664	S59637	glucose transport
18	86.5	7.4	459	T11398	NADH2 dehydrogenas
19	86	7.3	182	T19126	hypothetical prote
20	86	7.3	783	E89551	protein K04E7.2 [i
21	86	7.3	796	T37330	probable low-affin
22	85.5	7.3	486	AC0365	probable permease
23	85.5	7.3	832	A40205	Na+/H+-exchanging
24	85	7.3	605	A36361	glucose transport
25	84	7.2	463	AB0807	phosphoglycerate t
26	83.5	7.1	912	T49399	hypothetical prote
27	83	7.1	157	G02355	tumor-associated m
28	83	7.1	375	A64183	xylose transport p
29	83	7.1	395	S73531	CDP-diglyceride sy

30	83	7.1	523	2	D83631	probable sulfate t
31	82.5	7.0	375	2	B40205	Na+/H+-exchanging
32	82.5	7.0	479	2	T29720	hypothetical prote
33	82	7.0	458	2	T11528	NADH2 dehydrogenas
34	82	7.0	458	2	B99613	NADH dehydrogenase
35	82	7.0	480	2	G86285	hypothetical prote
36	81	6.9	458	2	B90615	NADH dehydrogenase
37	81	6.9	552	2	S47034	cell fusion protei
38	80.5	6.9	341	2	T23116	hypothetical prote
39	80.5	6.9	386	2	AF2687	conserved hypothet
40	80.5	6.9	391	2	B97469	probable membrane
41	80.5	6.9	415	2	AC0567	probable metabolit
42	80.5	6.9	665	2	A53582	Na+/glucose cotran
43	80.5	6.9	994	2	S19595	chloride channel p
44	80	6.8	300	2	B69072	hypothetical prote
45	80	6.8	437	2	T47831	hypothetical prote

ALIGNMENTS

RESULT 1
A39484
androgen-withdrawal apoptosis protein RVP1, prostatic - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 04-Mar-2000
C;Accession: A39484
R;Briehl, M.M.; Miesfeld, R.L.
Mol. Endocrinol. 5, 1381-1388, 1991
A;Title: Isolation and characterization of transcripts induced by androgen withdrawal an
A;Reference number: A39484; MUID:92130987; PMID:1723140
A;Accession: A39484
A;Molecule type: mRNA
A;Residues: 1-280 <BRI>
A;Cross-references: GB:M74067; NID:g205857; PIDN:AAA41760.1; PID:g205858
C;Genetics:
A;Gene: RVP.1
C;Superfamily: rat androgen-withdrawal apoptosis protein RVP1

Query Match 41.7%; Score 489; DB 2; Length 280;
Best Local Similarity 42.6%; Pred. No. 2e-39;
Matches 100; Conservative 41; Mismatches 72; Indels 22; Gaps 4;

Qy	5	AL E I A G L F L G G V M G T V A V T M P Q W R V S A F I E N N I V V F E N F W E G L W M N C V R Q A N I R M Q C	64
Db	4	S L E I T G T S L A V L G W L C T I V C C A L P M W R V S A F I G S S I I T A Q I T W E G L W M N C V - Q S T G Q M Q C	62
Qy	65	K I Y D S L L A L S P D L Q A A R G L M C A A S V M S F L A F M M A I L G M K T R C T G D N E K V K A H I L L T A G I	124
Db	63	K M Y D S L L A L P Q D L Q A A R A L I V V S I L L A A F G L L V A L V G A Q C T N C V Q D - E T A K A K I T I V A G V	121
Qy	125	I F I I T G M V V L I P V S W V A N A I I R D F Y N S I V N V A Q K R E L G E A L Y L G W T T A L V L I V G G A L F C C	184
Db	122	L F L L A A V L T L V P V S W S A N T I I R D F Y N P L V P E A Q K R E M G T G L Y V G W A A A L Q L L G G A L L C C	181
Qy	185	V F C C N E K S S S Y R - - Y S I P - - - - - S H R T T Q K S Y H T G K K S P S V Y	219
Db	182	S C P P R E K Y A P T K I L Y S A P R S T G P G T G T A Y D R K T T S E R P G A R T P H H H Y Q P S M Y	236

RESULT 2
A44432
amino acid transport protein - pig
N;Alternate names: Na+/amino acid cotransporter, SAAT1
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
C;Accession: A44432
R;Kong, C.T.; Yet, S.F.; Lever, J.E.
J. Biol. Chem. 268, 1509-1512, 1993
A;Title: Cloning and expression of a mammalian Na+/amino acid cotransporter with sequenc
A;Reference number: A44432; MUID:93131881; PMID:8420925
A;Accession: A44432
A;Molecule type: nucleic acid

A;Residues: 1-660 <KON>
A;Cross-references: GB:L02900; NID:g164666; PIDN:AAC37325.1; PID:g164667
A;Experimental source: kidney epithelial cell line LLC-PK1
A;Note: sequence extracted from NCBI backbone (NCBIP:122778)
C;Superfamily: proline carrier protein
C;Keywords: amino acid transport; membrane protein

Query Match 8.6%; Score 100.5; DB 2; Length 660;
Best Local Similarity 27.0%; Pred. No. 0.11;
Matches 38; Conservative 23; Mismatches 55; Indels 25; Gaps 6;

QY 54 CVRQANIRMQCKIYD-SLLALSPDLQAARGLMCAASVMSFLAFMMAILGKMKTRCTGD-- 110
Db 351 CVKHCGTEVGCNSYAYPLLVMEMLPMSGLRGLMLSVMLASLMSLSLTSIFNSASTLFTMDLY 410
QY 111 ---NEKVKAHILLTAGIIFIITGMVVLPVSWVANAIIRDFYNSIVNVAQKRELGEAL-- 165
Db 411 TKIRKQASEKELLIIAGRLFI--LLIVISIVWV-----PLVQVAQNGQLFHYIES 458
QY 166 ---YLGWTTALVLIVGGALFC 183
Db 459 ISSYLGPPPIAAVFLL--AIFC 477

RESULT 3
A49182
integral membrane protein MP20 - rat
N;Alternate names: lens membrane protein MP20
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C;Accession: A49182; S27883
R;Kumar, N.M.; Jarvis, L.J.; Tenbroek, E.; Louis, C.F.
Exp. Eye Res. 56, 35-43, 1993
A;Title: Cloning and expression of a major rat lens membrane protein, MP20.
A;Reference number: A49182; MUID:93162128; PMID:7679355
A;Accession: A49182
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-173 <KUM>
A;Cross-references: GB:S55224; NID:g265405; PIDN:AAB25334.1; PID:g265406
A;Experimental source: lens
A;Note: sequence extracted from NCBI backbone (NCBIN:124760, NCBIP:124761)
R;Kumar, N.M.; Jarvis, L.J.; Tenbroek, E.; Louis, C.F.
submitted to the EMBL Data Library, February 1992
A;Description: Cloning and expression of a major lens membrane protein, MP20.
A;Reference number: S27883
A;Accession: S27883
A;Molecule type: mRNA
A;Residues: 1-173 <KUM2>
A;Cross-references: EMBL:M87053; NID:g205514; PIDN:AAA41631.1; PID:g205515
C;Superfamily: growth arrest-specific protein
C;Keywords: membrane protein

Query Match 8.5%; Score 99.5; DB 2; Length 173;
Best Local Similarity 21.9%; Pred. No. 0.035;
Matches 43; Conservative 25; Mismatches 75; Indels 53; Gaps 9;

QY 10 GLFLGGVGMVGTAVVTMPQW---RVSAFIENNVVFNFWFEGLMWNCVVRQANIRMQCKI 66
Db 8 GLFCAWVGTILLVVATATDTHWMQYRLSCSFAH-----QGLWRYCLGN-----KCFL 53
QY 67 YDSLLALSPDLQAARGLM-----CAAS--VMSFLAFMMAILGKMKTRCTGDNEKVKAHIL 119
Db 54 QTESIAY---WNATRAFMILSALCATSGIIMGVLAFAQQSTFTRLSR-----P 98
QY 120 LTAGIIFIITGMVVLPVSWVANAIIRDFYNSIVNVAQKRELGE-----ALYLGWTTALV 174
Db 99 FSAGIMFFASTLFLVLLALA-----ITYGTVTSVFLGRFRFGDWFESWSYILGWVALLM 149
QY 175 LIVGGALFCCVFCNE 190
Db 150 TFFAGIFYMCAYRME 165

RESULT 4
S10196
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - chicken mitochondrion
C;Species: mitochondrion Gallus gallus (chicken)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Jun-2002
C;Accession: S10196
R;Desjardins, P.; Morais, R.
J. Mol. Biol. 212, 599-634, 1990
A;Title: Sequence and gene organization of the chicken mitochondrial genome. A novel gen
A;Reference number: S10187; MUID:90230301; PMID:2329578
A;Accession: S10196
A;Molecule type: DNA
A;Residues: 1-459 <DES>
A;Cross-references: EMBL:X52392; NID:g12960; PIDN:CAA36634.1; PID:g12970
C;Genetics:
A;Gene: ND4
A;Genome: mitochondrion
A;Genetic code: SGC1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 8.3%; Score 97.5; DB 2; Length 459;
Best Local Similarity 23.7%; Pred. No. 0.15;
Matches 51; Conservative 45; Mismatches 86; Indels 33; Gaps 12;

QY 11 LFLGGVGMVGTAVVTMPQWRVSFAFIENNVVFNFWFEGLMWN--CVRQANIRMQCKIYD 68
Db 236 LKLGGYGI---MRVTLLME-PVSNFLHYPFLLA-LWGALMTSSICLRQTDLK----- 283
QY 69 SLLALSPDLQAARGLMCAASVM----SFLAFMMAILGKMKCTR----CTGDNEKVKAH--- 117
Db 284 SLIAYSS--VSHMGLVIAASMIQTQWSFGAMILMISHGLTSSLLFCLANTINVERTHSRI 341
QY 118 ILLTAGIIFIITGMVVLPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIV 177
Db 342 LILTRG---LQPLPLMSVWLLANLTNLMALPPTTNLMAELTIMVALF-NWSSPTIILT 396
QY 178 GGA-LFCCVFCCKNEKSSSVRYSIIPSHRTTQKSYHT 211
Db 397 GTATLLTASYTLYMLLSTQRTGLPSHITTPNSNT 431

RESULT 5
A48300
lens membrane protein MP19 - bovine
N;Alternate names: lens fiber cell membrane protein MP18; lens fiber membrane intrinsic
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 11-Jan-2000
C;Accession: A48300; A34490; S05010
R;Gutekunst, K.A.; Rao, G.N.; Church, R.L.
Curr. Eye Res. 9, 955-961, 1990
A;Title: Molecular cloning and complete nucleotide sequence of the cDNA encoding a bovin
A;Reference number: A48300; MUID:91114349; PMID:2276272
A;Accession: A48300
A;Molecule type: mRNA
A;Residues: 1-173 <GUT>
A;Cross-references: GB:I04188; NID:g163294; PIDN:AAA30621.1; PID:g163295
R;Louis, C.F.; Hur, K.C.; Galvan, A.C.; TenBroek, E.M.; Jarvis, L.J.; Eccleston, E.D.; H
J. Biol. Chem. 264, 19967-19973, 1989
A;Title: Identification of an 18,000-dalton protein in mammalian lens fiber cell membra
A;Reference number: A34490; MUID:90062105; PMID:2584203
A;Accession: A34490
A;Molecule type: protein
A;Residues: 1-23 <LOU>
A;Experimental source: lens
R;Rao, G.N.; Gutekunst, K.A.; Church, R.L.
FEBS Lett. 250, 483-486, 1989
A;Title: Bovine lens 23, 21 and 19 kDa intrinsic membrane proteins have an identical am
A;Reference number: S05010; MUID:89325619; PMID:2473922
A;Accession: S05010
A;Molecule type: protein
A;Residues: 1-20 <RAO>

QY 1 MATHALEIAGL-----FLGGVGMVGTVAVTMPQWRVSAFIENN----- 39
Db 386 LAKHRLLYPGIVTFVIASTFPFGMGQFMAGELMPREAISTLFDNNNTWKHAGDPESLGQ 445
QY 40 -----IVVPENFWEGLWMNCVRQANIRMQC-----KIYDSLLA- 72
Db 446 SAVWIHPRVNVVILIFFVMKFWMSIV-ATTMPICGGFMPVFLGAAGRLVGEIMAM 504
QY 73 LSPDLQAARGLMCAASVMSFLAFMMAILGKMKTRCTGDNEKVKAHILLTAGIIFIITG-- 130
Db 505 LFPD-----GILFDDIYKILPGGYAVIG--AAALTG---AVSHTVSTAVICFELTGQI 553
QY 131 -----MVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGW 169
Db 554 AHILPMVAVILANMVAQSLQPSLYDSIIQVKLPYLPD---LGW 595

RESULT 12
AH0781
probable membrane protein STY2426 [imported] - Salmonella enterica subsp. enterica serov
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AH0781
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AH0781
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-380 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD02574.1; PID:gl6503432; GSPDB:GN00176
C;Genetics:
A;Gene: STY2426

Query Match 7.6%; Score 89.5; DB 2; Length 380;
Best Local Similarity 20.3%; Pred. No. 0.71;
Matches 50; Conservative 41; Mismatches 82; Indels 73; Gaps 12;

QY 12 FLGGVGMVGTVAVTM-----PQWRVSAFIENNIIVVFENFWEGLWMNCVRQANI 60
Db 9 FVRGVAILGILLNISAFGLPKAAYLNPAW-----YGAIVPEDAWSMAILDIVAQKF 61
QY 61 RMQCKIYDLSLLALSPDLQAARG---LMCAASVMSFLAFMMA-----ILGKMC 104
Db 62 ---LTLFALLFGAGLQMLPRGKQWQISRLTLVLGLGFHAFHFFWDGDLILAYGLVLIC 118
QY 105 TRCTGDNEKVKAHILLTAGIIFIITGMVVLIPV-----SWV--ANAIIRDFY--- 149
Db 119 WRLVRDAPSVKS--LFNTGILLYLVGIGVLLLVGVSSSETSRATPDASAILYEKYWK 176
QY 150 ----NSIVNVAQKRE---LGEALYLGWTTALVILVGGALFCCVCCNEKSSSY---RYSI 199
Db 177 NGGMEAISNRAEMLSNSLLALGAQYQWQLAGMILLGAALM-----RSGWLKGQYSL 227
QY 200 PSHRTT 205
Db 228 RHYRRT 233

RESULT 13
T11358
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - Daphnia pulex mitochondrion
C;Species: mitochondrion Daphnia pulex
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
C;Accession: T11358
R;Crease, T.J.
Gene 233, 89-99, 1999
A;Title: The complete sequence of the mitochondrial genome of Daphnia pulex (Cladocera:

A;Reference number: Z17264; MUID:99307147; PMID:10375625
A;Accession: T11358
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-440 <CRE>
A;Cross-references: EMBL:AF117817; NID:g4927669; PID:g4927678; PIDN:AAD33238.1
C;Genetics:
A;Gene: ND4
A;Genome: mitochondrion
A;Genetic code: SGC4
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 7.6%; Score 89; DB 2; Length 440;
Best Local Similarity 23.7%; Pred. No. 0.93;
Matches 51; Conservative 29; Mismatches 51; Indels 84; Gaps 13;

QY 8 IAG--LFLGGVGMVGTVAVTMPQWRVSAFIENNIIVVFENFWEGLWM-----NCVRQ 57
Db 215 LAGVLLKLGGMV-----RVVPYIELSLSEFSSFLMSVSLVGGVTASVICIRQ 263
QY 58 ANIRMQCK---IYDS-----LLALSPDLQAARGL-----MCAASVMSFLAFMMA 98
Db 264 TD-----CKSLVAYSSVAHMAVLVLGVVINSVGLAGVVTIMISHGLCSSGLFSLVGMIEY 319
QY 99 ILGKMKTRCTGDNEKVKAHILLTAGIIFIITGMVVLIPVS---WVANAIIRDFYNSIVNV 155
Db 320 RMGTRS-----IILIRSLITLAPLSTLWM-----FLFAISNM 351
QY 156 A---QKRELGEALYL-----GWTALVLIVGGALF 182
Db 352 AAPSPNLLGE-IYLFISSIGWGGSSLLVGGLSF 385

RESULT 14
S33044
hypothetical protein - human herpesvirus 4
C;Species: human herpesvirus 4, Epstein-Barr virus
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
C;Accession: S33044
R;Farrell, P.J.
submitted to the EMBL Data Library, March 1988
A;Reference number: S32973
A;Accession: S33044
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-618 <FAR>
A;Cross-references: EMBL:V01555

Query Match 7.5%; Score 88; DB 2; Length 618;
Best Local Similarity 26.1%; Pred. No. 1.6;
Matches 37; Conservative 15; Mismatches 66; Indels 24; Gaps 4;

QY 61 RMQCKIYDLSLLALSPDLQAARGLMCAASVMSFL-----AFMMAILGM-----KCTRCT 108
Db 2 RAQCFALSSATCLITNLSAASSSSAAWSRVGFLGTCKRNSAKMLAHLNQVTRIPPCPPFS 61
QY 109 GDNEKVKAHILLTAGIIFIITGMVVLIPVSWVANAIIRDF--YNSIVNVAQKRELGEALYL 167
Db 62 GREARLKFFHFFSWSTFM-----LSWPNNTALREIRTRAATNLTHHPHLVDTLYH 110
QY 168 GWTALVLIVGGALFCCVCCN 189
Db 111 ASPQTPFLTRSGALYRFVTCN 132

RESULT 15
T23909
hypothetical protein R04F11.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 12-Jun-2003
C;Accession: T23909
R;Harris, B.

submitted to the EMBL Data Library, June 1996
A;Reference number: Z19816
A;Accession: T23909
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-297 <WIL>
A;Cross-references: EMBL:Z74475; PIDN:CAA98959.1; GSPDB:GN00023; CESP:R04F11.1
A;Experimental source: clone R04F11
C;Genetics:
A;Gene: CESP:R04F11.1
A;Map position: 5
A;Introns: 44/3; 82/3; 120/1; 156/1; 244/3
C;Superfamily: uncharacterized conserved protein K10D6.2b

Query Match		7.4%;	Score 87;	DB 2;	Length 297;
Best Local Similarity		21.7%;	Pred. No. 0.96;		
Matches	55;	Conservative	36;	Mismatches	83;
				Indels	80;
				Gaps	13;
QY	6	LEIAGLFLGGVGMGTAVTVMQWRVS	AFIENNVFENFWEGLMNCV-----	55	
Db	57	LLVTSIFLIVSGLILTAFLSPLWEVVD	FRSHL-----SHHGLWDCIVHHETLIPLH	112	
QY	56	-RQANIR-----MQCKIYDSI--	LALSPDLQAARGLMCAA-----	SWMSFLAF	95
Db	113	EDQAEIRGDRCDSKMDSSVQASLRVALE	KGDEEARELLHRFLPHKGVIFFAVFTFVFG	172	
QY	96	MMAILGMKCTRCTGDNEKVKAHILLTAG	IIFIITGMVVLIPVSWVANAIIRDFYNS----	151	
Db	173	LISILIGSCSPCFPPNA-----	LLYVGV--FMTGACSL-----ADIIYIFAFNQKPIF	220	
QY	152	-----IVNVAQKRE-----	LGEALYLGWTTTALVLIVG--GALFCCVF-----	186	
Db	221	TKEQSEPHQEVLSRRRERGSIGPIYKRL	GIATYMHMFSGMMLIAAFIFSIFCAYFLITSKH	280	
QY	187	-----CCNEKSSSYR	196		
Db	281	AHDVCCTSR-KEYR	293		

Search completed: September 1, 2004, 16:56:26
Job time : 19 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2004, 16:54:39 ; Search time 49 Seconds
(without alignments)
1444.651 Million cell updates/sec

Title: US-10-063-732-120
Perfect score: 1172
Sequence: 1 MATHALEIAGLFLGGVMVG.....QKSYHTGKKSPSVYRSQYV 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen parameters: 1297172

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1172	100.0	225	9	US-09-731-872-405
2	1172	100.0	225	10	US-09-946-374-328
3	1172	100.0	225	10	US-09-876-997-405
4	1172	100.0	225	12	US-10-206-915-358
5	1172	100.0	225	12	US-10-199-670-358
6	1172	100.0	225	12	US-10-201-858-358
7	1172	100.0	225	12	US-10-205-890-358
8	1172	100.0	225	12	US-10-208-024-358
9	1172	100.0	225	12	US-10-201-853-358
10	1172	100.0	225	12	US-10-063-745-120
11	1172	100.0	225	12	US-10-063-512-120
12	1172	100.0	225	12	US-10-063-513-120
13	1172	100.0	225	12	US-10-063-515-120
14	1172	100.0	225	12	US-10-063-549-120
15	1172	100.0	225	12	US-10-063-569-120

16	1172	100.0	225	12	US-10-063-551-120	Sequence 120, App
17	1172	100.0	225	12	US-10-174-581-358	Sequence 358, App
18	1172	100.0	225	12	US-10-176-483-358	Sequence 358, App
19	1172	100.0	225	12	US-10-176-749-358	Sequence 358, App
20	1172	100.0	225	12	US-10-176-914-358	Sequence 358, App
21	1172	100.0	225	12	US-10-176-915-358	Sequence 358, App
22	1172	100.0	225	12	US-10-006-485A-328	Sequence 328, App
23	1172	100.0	225	12	US-10-013-907A-328	Sequence 328, App
24	1172	100.0	225	12	US-10-015-499A-328	Sequence 328, App
25	1172	100.0	225	12	US-10-063-555-120	Sequence 120, App
26	1172	100.0	225	12	US-10-063-563-120	Sequence 120, App
27	1172	100.0	225	12	US-10-063-594-120	Sequence 120, App
28	1172	100.0	225	12	US-10-063-553-120	Sequence 120, App
29	1172	100.0	225	12	US-10-063-554-120	Sequence 120, App
30	1172	100.0	225	12	US-10-176-484-358	Sequence 358, App
31	1172	100.0	225	12	US-10-180-550-358	Sequence 358, App
32	1172	100.0	225	12	US-10-183-014-358	Sequence 358, App
33	1172	100.0	225	12	US-10-187-738-358	Sequence 358, App
34	1172	100.0	225	12	US-10-187-740-358	Sequence 358, App
35	1172	100.0	225	12	US-10-187-883-358	Sequence 358, App
36	1172	100.0	225	12	US-10-194-363-358	Sequence 358, App
37	1172	100.0	225	12	US-10-194-460-358	Sequence 358, App
38	1172	100.0	225	12	US-10-194-463-358	Sequence 358, App
39	1172	100.0	225	12	US-10-194-484-358	Sequence 358, App
40	1172	100.0	225	12	US-10-195-884-358	Sequence 358, App
41	1172	100.0	225	12	US-10-195-896-358	Sequence 358, App
42	1172	100.0	225	12	US-10-196-744-358	Sequence 358, App
43	1172	100.0	225	12	US-10-196-755-358	Sequence 358, App
44	1172	100.0	225	12	US-10-196-757-358	Sequence 358, App
45	1172	100.0	225	12	US-10-197-704-358	Sequence 358, App

ALIGNMENTS

RESULT 1
US-09-731-872-405
; Sequence 405, Application US/09731872
; Patent No. US20020102604A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78.US3.REG
; CURRENT APPLICATION NUMBER: US/09/731,872
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 405
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-731-872-405

Query Match	100.0%;	Score 1172;	DB 9;	Length 225;
Best Local Similarity	100.0%;	Pred. No. 4.9e-119;		
Matches	225;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1	MATHALEIAGLFLGGVMVGTVAVTMPQWRVSFAFIENNIVVFENFWEGLMNCVRQANI	60	
Db	1	MATHALEIAGLFLGGVMVGTVAVTMPQWRVSFAFIENNIVVFENFWEGLMNCVRQANI	60	
QY	61	RMQCKIYDSSLALSPDLQAARGLMCAASVMSFLAFMMAILGKCTCTGDNEKVKAHILL	120	
Db	61	RMQCKIYDSSLALSPDLQAARGLMCAASVMSFLAFMMAILGKCTCTGDNEKVKAHILL	120	
QY	121	TAGLIIFIITGMVILIPVSWVANAIIRDFFNSIVNVAOKRELGEALYLGWTTALVLIVGGA	180	

Db 121 TAGIIFIITGMVVLIPVSWVANAIIRDFFYNSIVNVAQKRELGEALVLGWTALVLIIVGGA 180
QY 181 LFCCVFCCKNEKSSSYRYSIPSHRITTKQSYHTGKKSPSVYRSQYV 225
Db 181 LFCCVFCCKNEKSSSYRYSIPSHRITTKQSYHTGKKSPSVYRSQYV 225

RESULT 2

US-09-946-374-328
; Sequence 328, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812

; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29

QY 61 RMOCKIYDSLALSPLDLOAARGLMCAASVMSFLAFEMMAILGMKCTRCTGDNEKVKAHILL 120

; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C513
; CURRENT APPLICATION NUMBER: US/10/206,915
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 358
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-206-915-358

Query Match 100.0%; Score 1172; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.9e-119;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNIIVVFENFWEGLMNCVRQANI 60
Db 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNIIVVFENFWEGLMNCVRQANI 60

QY 61 RMOCKIYDLSLLALSPDLQAARGLMCAASVMSFLAFMMAILGKMKCTRCTGDNEKVAHILL 120
Db 61 RMOCKIYDLSLLALSPDLQAARGLMCAASVMSFLAFMMAILGKMKCTRCTGDNEKVAHILL 120

QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTTALVLIVGGA 180
Db 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTTALVLIVGGA 180

QY 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPPSVYSRSQYV 225
Db 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPPSVYSRSQYV 225

RESULT 5
US-10-199-670-358
; Sequence 358, Application US/10199670
; Publication No. US20040033560A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C401
; CURRENT APPLICATION NUMBER: US/10/199,670
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 358
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-199-670-358

Query Match 100.0%; Score 1172; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.9e-119;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNIIVVFENFWEGLMNCVRQANI 60
Db 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNIIVVFENFWEGLMNCVRQANI 60

QY 61 RMOCKIYDLSLLALSPDLQAARGLMCAASVMSFLAFMMAILGKMKCTRCTGDNEKVAHILL 120
Db 61 RMOCKIYDLSLLALSPDLQAARGLMCAASVMSFLAFMMAILGKMKCTRCTGDNEKVAHILL 120

QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTTALVLIVGGA 180
Db 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTTALVLIVGGA 180

QY 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPPSVYSRSQYV 225
Db 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPPSVYSRSQYV 225

RESULT 6
US-10-201-858-358
; Sequence 358, Application US/10201858
; Publication No. US20040038337A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C464
; CURRENT APPLICATION NUMBER: US/10/201,858

```
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 358
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-201-858-358
```

```
Query Match      100.0%; Score 1172; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.9e-119;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATHALEIAGFLGGVGMVGTVAVTMPQWRVSAFIENNIIVVFENFWEGLMNCVRQANI 60
   |||||
Db 1 MATHALEIAGFLGGVGMVGTVAVTMPQWRVSAFIENNIIVVFENFWEGLMNCVRQANI 60

QY 61 RMQCKIYDSSLALSPDLQAARGLMCAASVMSFLAFMMAILGKCTRCTGDNEKVKAHILL 120
   |||||
Db 61 RMQCKIYDSSLALSPDLQAARGLMCAASVMSFLAFMMAILGKCTRCTGDNEKVKAHILL 120

QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
   |||||
Db 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180

QY 181 LFCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKSPSVYRSQYV 225
   |||||
Db 181 LFCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKSPSVYRSQYV 225
```

```
RESULT 7
US-10-205-890-358
; Sequence 358, Application US/10205890
; Publication No. US20040048334A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C519
; CURRENT APPLICATION NUMBER: US/10/205,890
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
```

```
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 358
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-205-890-358
```

```
Query Match      100.0%; Score 1172; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.9e-119;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATHALEIAGFLGGVGMVGTVAVTMPQWRVSAFIENNIIVVFENFWEGLMNCVRQANI 60
   |||||
Db 1 MATHALEIAGFLGGVGMVGTVAVTMPQWRVSAFIENNIIVVFENFWEGLMNCVRQANI 60

QY 61 RMQCKIYDSSLALSPDLQAARGLMCAASVMSFLAFMMAILGKCTRCTGDNEKVKAHILL 120
   |||||
Db 61 RMQCKIYDSSLALSPDLQAARGLMCAASVMSFLAFMMAILGKCTRCTGDNEKVKAHILL 120

QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
   |||||
Db 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180

QY 181 LFCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKSPSVYRSQYV 225
   |||||
Db 181 LFCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKSPSVYRSQYV 225
```

```
RESULT 8
US-10-208-024-358
; Sequence 358, Application US/10208024
; Publication No. US20040048335A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C538
; CURRENT APPLICATION NUMBER: US/10/208,024
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
```

```
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 358
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-208-024-358

Query Match      100.0%; Score 1172; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.9e-119;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNIIVFENFWEGLWMNCVRQANI 60
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNIIVFENFWEGLWMNCVRQANI 60

QY 61 RMOCKIYDLSLLALSPDLQAARGLMCAASVMSFLAFMMAILGKCTRCTGDNEKVKAHILL 120
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 RMOCKIYDLSLLALSPDLQAARGLMCAASVMSFLAFMMAILGKCTRCTGDNEKVKAHILL 120

QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVLIIVGGA 180
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 TAGIIFIITGMVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVLIIVGGA 180

QY 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPPSVYSRSQYV 225
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPPSVYSRSQYV 225

RESULT 9
US-10-201-853-358
; Sequence 358, Application US/10201853
; Publication No. US20040053358A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C465
; CURRENT APPLICATION NUMBER: US/10/201,853
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
```

```
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 358
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-201-853-358

Query Match      100.0%; Score 1172; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.9e-119;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNIIVFENFWEGLWMNCVRQANI 60
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNIIVFENFWEGLWMNCVRQANI 60

QY 61 RMOCKIYDLSLLALSPDLQAARGLMCAASVMSFLAFMMAILGKCTRCTGDNEKVKAHILL 120
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 RMOCKIYDLSLLALSPDLQAARGLMCAASVMSFLAFMMAILGKCTRCTGDNEKVKAHILL 120

QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVLIIVGGA 180
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 TAGIIFIITGMVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVLIIVGGA 180

QY 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPPSVYSRSQYV 225
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPPSVYSRSQYV 225

RESULT 10
US-10-063-745-120
; Sequence 120, Application US/10063745
; Publication No. US20040058411A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,745
; CURRENT FILING DATE: 2002-05-09
; PRIOR APPLICATION removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 120
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-745-120

Query Match      100.0%; Score 1172; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.9e-119;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNIIVFENFWEGLWMNCVRQANI 60
```

```
Db      1 MATHALEIAGLFLGGVGMGTVAVTMPQWRVSAFIENNIIVVFENFWEGLMWNCVRQANI 60
QY      61 RMOCKIYDLSLLALSPDLQAARGLMCAASVMSFLAFMAILGKMKTRCTGDNEKVKKAHILL 120
Db      61 RMOCKIYDLSLLALSPDLQAARGLMCAASVMSFLAFMAILGKMKTRCTGDNEKVKKAHILL 120
QY      121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIIVGGA 180
Db      121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIIVGGA 180
QY      181 LFCCVFCCKNEKSSSYRYSIPSHRRTTQKSYHTGKKSPSVYSRSQYV 225
Db      181 LFCCVFCCKNEKSSSYRYSIPSHRRTTQKSYHTGKKSPSVYSRSQYV 225
```

```
RESULT 11
US-10-063-512-120
; Sequence 120, Application US/10063512
; Publication No. US20030018183A1
; GENERAL INFORMATION:
; APPLICANT: Eaton,Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,512
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 120
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-512-120
```

```
Query Match      100.0%; Score 1172; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.9e-119;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MATHALEIAGLFLGGVGMGTVAVTMPQWRVSAFIENNIIVVFENFWEGLMWNCVRQANI 60
Db      1 MATHALEIAGLFLGGVGMGTVAVTMPQWRVSAFIENNIIVVFENFWEGLMWNCVRQANI 60
QY      61 RMOCKIYDLSLLALSPDLQAARGLMCAASVMSFLAFMAILGKMKTRCTGDNEKVKKAHILL 120
Db      61 RMOCKIYDLSLLALSPDLQAARGLMCAASVMSFLAFMAILGKMKTRCTGDNEKVKKAHILL 120
QY      121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIIVGGA 180
Db      121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIIVGGA 180
QY      181 LFCCVFCCKNEKSSSYRYSIPSHRRTTQKSYHTGKKSPSVYSRSQYV 225
Db      181 LFCCVFCCKNEKSSSYRYSIPSHRRTTQKSYHTGKKSPSVYSRSQYV 225
```

```
RESULT 12
US-10-063-513-120
; Sequence 120, Application US/10063513
; Publication No. US20030018172A1
; GENERAL INFORMATION:
; APPLICANT: Eaton,Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
```

```
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,513
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 120
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-513-120
```

```
Query Match      100.0%; Score 1172; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.9e-119;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MATHALEIAGLFLGGVGMGTVAVTMPQWRVSAFIENNIIVVFENFWEGLMWNCVRQANI 60
Db      1 MATHALEIAGLFLGGVGMGTVAVTMPQWRVSAFIENNIIVVFENFWEGLMWNCVRQANI 60
QY      61 RMOCKIYDLSLLALSPDLQAARGLMCAASVMSFLAFMAILGKMKTRCTGDNEKVKKAHILL 120
Db      61 RMOCKIYDLSLLALSPDLQAARGLMCAASVMSFLAFMAILGKMKTRCTGDNEKVKKAHILL 120
QY      121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIIVGGA 180
Db      121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIIVGGA 180
QY      181 LFCCVFCCKNEKSSSYRYSIPSHRRTTQKSYHTGKKSPSVYSRSQYV 225
Db      181 LFCCVFCCKNEKSSSYRYSIPSHRRTTQKSYHTGKKSPSVYSRSQYV 225
```

```
RESULT 13
US-10-063-515-120
; Sequence 120, Application US/10063515
; Publication No. US20030018173A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,515
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 120
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-515-120
```

```
Query Match      100.0%; Score 1172; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.9e-119;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MATHALEIAGLFLGGVGMGTVAVTMPQWRVSAFIENNIIVVFENFWEGLMWNCVRQANI 60
Db      1 MATHALEIAGLFLGGVGMGTVAVTMPQWRVSAFIENNIIVVFENFWEGLMWNCVRQANI 60
```


QY	61	RMQCKIYD	SL	LL	AL	SP	DL	QA	AR	GL	MC	AA	SV	MS	FL	AF	MM	AI	LG	MK	CT	RC	TG	DN	EK	VK	AH	IL	120																						
Db	61	RMQCKIYD	SL	LL	AL	SP	DL	QA	AR	GL	MC	AA	SV	MS	FL	AF	MM	AI	LG	MK	CT	RC	TG	DN	EK	VK	AH	IL	120																						
QY	121	TAGIIFIIT	G	M	V	V	L	I	P	V	S	W	A	N	A	I	R	D	F	Y	N	S	I	V	N	V	A	Q	K	R	E	L	G	E	A	L	Y	L	G	W	T	T	A	L	V	L	I	V	G	A	180
Db	121	TAGIIFIIT	G	M	V	V	L	I	P	V	S	W	A	N	A	I	R	D	F	Y	N	S	I	V	N	V	A	Q	K	R	E	L	G	E	A	L	Y	L	G	W	T	T	A	L	V	L	I	V	G	A	180
QY	181	LFCCVFC	C	N	E	K	S	S	S	Y	R	I	S	I	P	S	H	R	T	T	Q	K	S	Y	H	T	G	K	K	S	P	S	V	V	S	R	S	Q	Y	V	225										
Db	181	LFCCVFC	C	N	E	K	S	S	Y	R	I	S	I	P	S	H	R	T	T	Q	K	S	Y	H	T	G	K	K	S	P	S	V	V	S	R	S	Q	Y	V	225											

RESULT 14

```

US-10-063-549-120
; Sequence 120, Application US/10063549
; Publication No. US20030027986A1
; GENERAL INFORMATION:
;   APPLICANT: Eaton, Dan L.
;   APPLICANT: Filvaroff, Ellen
;   APPLICANT: Gerritsen, Mary E.
;   APPLICANT: Goddard, Audrey
;   APPLICANT: Godowski, Paul J.
;   APPLICANT: Grimaldi, Christopher J.
;   APPLICANT: Gurney, Austin L.
;   APPLICANT: Watanabe, Colin K.
;   APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,549
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 120
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-063-549-120

```

[illegible]

RESULT 15

US-10-063-569-120
; Sequence 120, Application US/10063569
; Publication No. US20030018168A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.

; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 869
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-258-869

Query Match 4.0%; Score 9; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 WEGWMNCV 55
|||
Db 10 WEGWMNCV 18

RESULT 3

US-09-205-258-344
; Sequence 344, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: PZ007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06

```
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 344
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (202)
; OTHER INFORMATION: Xaa equals stop translation
US-09-205-258-344
```

```
Query Match      4.0%; Score 9; DB 4; Length 202;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches      9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      47 WEGLWMNCV 55
Db      39 WEGLWMNCV 47

RESULT 4
US-09-603-552-13
; Sequence 13, Application US/09603552
; Patent No. 6590089
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Tang, Y. Tom
; APPLICANT: Patterson, Chandra
; TITLE OF INVENTION: RVP-1 VARIANT DIFFERENTIALLY EXPRESSED IN CROHN'S DISEASE
; FILE REFERENCE: PC-0016 US
; CURRENT APPLICATION NUMBER: US/09/603,552
; CURRENT FILING DATE: 2000-06-22
```

```
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank No. 6590089 g2570129
US-09-603-552-13
```

```
Query Match      4.0%; Score 9; DB 4; Length 220;
Best Local Similarity 100.0%; Pred. No. 0.78;
Matches      9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      47 WEGLWMNCV 55
Db      46 WEGLWMNCV 54
```

```
RESULT 5
US-09-130-491-15
; Sequence 15, Application US/09130491
; Patent No. 6416974
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
; FILE REFERENCE: 09404/041001
; CURRENT APPLICATION NUMBER: US/09/130,491
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: US 60/058,108
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: US 60/054,961
; EARLIER FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-130-491-15
```

```
Query Match      4.0%; Score 9; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches      9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      47 WEGLWMNCV 55
Db      46 WEGLWMNCV 54
```

```
RESULT 6
US-09-489-039A-13977
; Sequence 13977, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13977
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13977

Query Match      3.6%; Score 8; DB 4; Length 225;
```

Fri Sep 3 10:15:54 2004

us-10-063-732-120.olig6.ra

```
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 TTALVLIV 177
Db 199 TTALVLIV 206

RESULT 7
US-09-252-991A-22253
; Sequence 22253, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22253
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22253

Query Match 3.6%; Score 8; DB 4; Length 420;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 173 LVLIVGGA 180
Db 300 LVLIVGGA 307

RESULT 8
US-09-589-567-2
; Sequence 2, Application US/09589567
; Patent No. 6479730
; GENERAL INFORMATION:
; APPLICANT: Mahajan, Pramod B.
; APPLICANT: Shi, Jinrui
; TITLE OF INVENTION: Maize DNA Ligase II Orthologue and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 1125
; CURRENT APPLICATION NUMBER: US/09/589,567
; CURRENT FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: US 60/145,911
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1218
; TYPE: PRT
; ORGANISM: Zea Mays
US-09-589-567-2

Query Match 3.6%; Score 8; DB 4; Length 1218;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 SLLALSPD 76
Db 623 SLLALSPD 630

RESULT 9
US-08-940-095-226
; Sequence 226, Application US/08940095
```

```
; Patent No. 6004925
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,095
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 226:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6004925e
US-08-940-095-226

Query Match 3.1%; Score 7; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 159 RELGEAL 165
Db 7 RELGEAL 13

RESULT 10
US-08-940-093-226
; Sequence 226, Application US/08940093
; Patent No. 6037323
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
```


STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,093
FILING DATE: 29-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 226:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6037323e
US-08-940-093-226

Query Match 3.1%; Score 7; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 159 RELGEAL 165
Db 7 RELGEAL 13

RESULT 11
US-08-940-096-226
Sequence 226, Application US/08940096
Patent No. 6046166
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,096
FILING DATE: 29-SEP-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0005-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 226:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6046166e
US-08-940-096-226

Query Match 3.1%; Score 7; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 159 RELGEAL 165
Db 7 RELGEAL 13

RESULT 12
US-09-465-719-226
Sequence 226, Application US/09465719
Patent No. 6265377
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/465,719
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,093
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 226:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6265377e

US-09-465-719-226

Query Match 3.1%; Score 7; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 159 RELGEAL 165
|||||
Db 7 RELGEAL 13

RESULT 13

US-09-453-605-226
; Sequence 226, Application US/09453605
; Patent No. 6329341
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,605
; FILING DATE: 26-No. 6329341-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 226:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6329341e
; SEQUENCE DESCRIPTION: SEQ ID NO: 226:
US-09-453-605-226

Query Match 3.1%; Score 7; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 159 RELGEAL 165
|||||
Db 7 RELGEAL 13

RESULT 14

US-09-453-838-226

; Sequence 226, Application US/09453838
; Patent No. 6376464
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,838
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 226:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6376464e
; US-09-453-838-226

Query Match 3.1%; Score 7; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 159 RELGEAL 165
|||||
Db 7 RELGEAL 13

RESULT 15

US-08-940-136-226
; Sequence 226, Application US/08940136
; Patent No. 6518412
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; Dufourcq, Jean
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
; USE TO TREAT DYSLIPIDEMIC DISORDERS.
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,136
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0007-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 226:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6518412e
US-08-940-136-226

```

```

Query Match      3.1%; Score 7; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      159 RELGEAL 165
      |||||
Db       7 RELGEAL 13

```

Search completed: September 1, 2004, 17:00:12
Job time : 21 secs

115771
Chapman
1911

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2004, 16:58:25 ; Search time 49 Seconds
(without alignments)
1444.651 Million cell updates/sec

Title: US-10-063-732-120
Perfect score: 225
Sequence: 1 MATHALEIAGLFLGGVGMVG.....QKSYHTGKSPSVYSRSQYV 225

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1297172 seqs, 314612898 residues

Word size : 6
Total number of hits satisfying chosen parameters: 5827

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	225	100.0	225	9	US-09-731-872-405
2	225	100.0	225	10	US-09-946-374-328
3	225	100.0	225	10	US-09-876-997-405
4	225	100.0	225	12	US-10-206-915-358
5	225	100.0	225	12	US-10-199-670-358
6	225	100.0	225	12	US-10-201-858-358
7	225	100.0	225	12	US-10-205-890-358
8	225	100.0	225	12	US-10-208-024-358
9	225	100.0	225	12	US-10-201-853-358
10	225	100.0	225	12	US-10-063-745-120
11	225	100.0	225	12	US-10-063-512-120
12	225	100.0	225	12	US-10-063-513-120
13	225	100.0	225	12	US-10-063-515-120
14	225	100.0	225	12	US-10-063-549-120
15	225	100.0	225	12	US-10-063-569-120

16	225	100.0	225	12	US-10-063-551-120	Sequence 120, App
17	225	100.0	225	12	US-10-174-581-358	Sequence 358, App
18	225	100.0	225	12	US-10-176-483-358	Sequence 358, App
19	225	100.0	225	12	US-10-176-749-358	Sequence 358, App
20	225	100.0	225	12	US-10-176-914-358	Sequence 358, App
21	225	100.0	225	12	US-10-176-915-358	Sequence 358, App
22	225	100.0	225	12	US-10-006-485A-328	Sequence 328, App
23	225	100.0	225	12	US-10-013-907A-328	Sequence 328, App
24	225	100.0	225	12	US-10-015-499A-328	Sequence 328, App
25	225	100.0	225	12	US-10-063-555-120	Sequence 120, App
26	225	100.0	225	12	US-10-063-563-120	Sequence 120, App
27	225	100.0	225	12	US-10-063-594-120	Sequence 120, App
28	225	100.0	225	12	US-10-063-553-120	Sequence 120, App
29	225	100.0	225	12	US-10-063-554-120	Sequence 120, App
30	225	100.0	225	12	US-10-176-484-358	Sequence 358, App
31	225	100.0	225	12	US-10-180-550-358	Sequence 358, App
32	225	100.0	225	12	US-10-183-014-358	Sequence 358, App
33	225	100.0	225	12	US-10-187-738-358	Sequence 358, App
34	225	100.0	225	12	US-10-187-740-358	Sequence 358, App
35	225	100.0	225	12	US-10-187-883-358	Sequence 358, App
36	225	100.0	225	12	US-10-194-363-358	Sequence 358, App
37	225	100.0	225	12	US-10-194-460-358	Sequence 358, App
38	225	100.0	225	12	US-10-194-463-358	Sequence 358, App
39	225	100.0	225	12	US-10-194-484-358	Sequence 358, App
40	225	100.0	225	12	US-10-195-884-358	Sequence 358, App
41	225	100.0	225	12	US-10-195-896-358	Sequence 358, App
42	225	100.0	225	12	US-10-196-744-358	Sequence 358, App
43	225	100.0	225	12	US-10-196-755-358	Sequence 358, App
44	225	100.0	225	12	US-10-196-757-358	Sequence 358, App
45	225	100.0	225	12	US-10-197-704-358	Sequence 358, App

ALIGNMENTS

RESULT 1
US-09-731-872-405
; Sequence 405, Application US/09731872
; Patent No. US20020102604A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78.US3.REG
; CURRENT APPLICATION NUMBER: US/09/731,872
; CURRENT FILING DATE: 2000-12-07
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 405
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-731-872-405

Query Match 100.0%; Score 225; DB 9; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.1e-208;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATHALEIAGLFLGGVGMVGTAVTVMPOQRVSAPFIENNVVFENFWEGLMNCVRQANI 60
|||||
Db 1 MATHALEIAGLFLGGVGMVGTAVTVMPOQRVSAPFIENNVVFENFWEGLMNCVRQANI 60
|||||

QY 61 RMCKIYDLSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120
|||||

Db 61 RMCKIYDLSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120
|||||

QY 121 TAGLIIFIITGMVLLIPVSWVANAIIRDFFNSIVNVAQKRELGEALYLCWTTALVLIVGGA 180
|||||

Db 121 TAGIIFIITGMVVLIPVSVWANAIIRDFFYNSIVNVAQKRELGEALYLGWTTALVLIIVGA 180
QY 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYRSQYV 225
Db 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYRSQYV 225

RESULT 2
US-09-946-374-328
; Sequence 328, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812

; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29


```
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C513
; CURRENT APPLICATION NUMBER: US/10/206,915
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 358
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-206-915-358

Query Match 100.0%; Score 225; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.1e-208;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSFAFIENNIIVVFENFWEGLMNCVRQANI 60
Db 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSFAFIENNIIVVFENFWEGLMNCVRQANI 60

QY 61 RMOCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120
Db 61 RMOCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120

QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGA 180
Db 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGA 180

QY 181 LFCCVFCCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYRSQYV 225
Db 181 LFCCVFCCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYRSQYV 225

RESULT 5
US-10-199-670-358
; Sequence 358, Application US/10199670
; Publication No. US20040033560A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C464
; CURRENT APPLICATION NUMBER: US/10/201,858
```

```
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C401
; CURRENT APPLICATION NUMBER: US/10/199,670
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 358
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-199-670-358

Query Match 100.0%; Score 225; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.1e-208;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSFAFIENNIIVVFENFWEGLMNCVRQANI 60
Db 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSFAFIENNIIVVFENFWEGLMNCVRQANI 60

QY 61 RMOCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120
Db 61 RMOCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120

QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGA 180
Db 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGA 180

QY 181 LFCCVFCCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYRSQYV 225
Db 181 LFCCVFCCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYRSQYV 225

RESULT 6
US-10-201-858-358
; Sequence 358, Application US/10201858
; Publication No. US20040038337A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C464
; CURRENT APPLICATION NUMBER: US/10/201,858
```

```

; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 358
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-201-858-358

Query Match      100.0%; Score 225; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.le-208;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNIIVVFENFWEGLMNCVRQANI 60
Db 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNIIVVFENFWEGLMNCVRQANI 60

QY 61 RMOCKIYDSSLALSPDLQAARGLMCAASVMSFLAFMMAILGKCTRCTGDNKVKAHILL 120
Db 61 RMOCKIYDSSLALSPDLQAARGLMCAASVMSFLAFMMAILGKCTRCTGDNKVKAHILL 120

QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
Db 121 TAGIIFIITGMVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180

QY 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYRSQYV 225
Db 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYRSQYV 225
```

```

RESULT 7
US-10-205-890-358
; Sequence 358, Application US/10205890
; Publication No. US20040048334A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C519
; CURRENT APPLICATION NUMBER: US/10/205,890
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
```

```

; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 358
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-205-890-358

Query Match      100.0%; Score 225; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.le-208;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNIIVVFENFWEGLMNCVRQANI 60
Db 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNIIVVFENFWEGLMNCVRQANI 60

QY 61 RMOCKIYDSSLALSPDLQAARGLMCAASVMSFLAFMMAILGKCTRCTGDNKVKAHILL 120
Db 61 RMOCKIYDSSLALSPDLQAARGLMCAASVMSFLAFMMAILGKCTRCTGDNKVKAHILL 120

QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
Db 121 TAGIIFIITGMVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180

QY 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYRSQYV 225
Db 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYRSQYV 225
```

```

RESULT 8
US-10-208-024-358
; Sequence 358, Application US/10208024
; Publication No. US20040048335A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C538
; CURRENT APPLICATION NUMBER: US/10/208,024
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
```

```

; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 358
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-208-024-358

Query Match      100.0%; Score 225; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.1e-208;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATHALEIAGLFLGGVGMVGTAVTVMPPQWRVSFAFIENNIIVVFENFWEGLWMNCVRQANI 60
Db 1 MATHALEIAGLFLGGVGMVGTAVTVMPPQWRVSFAFIENNIIVVFENFWEGLWMNCVRQANI 60

QY 61 RMQCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120
Db 61 RMQCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120

QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVLIIVGGA 180
Db 121 TAGIIFIITGMVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVLIIVGGA 180

QY 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV 225
Db 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV 225

RESULT 10
US-10-063-745-120
; Sequence 120, Application US/10063745
; Publication No. US20040058411A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,745
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 120
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-063-745-120

Query Match      100.0%; Score 225; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.1e-208;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATHALEIAGLFLGGVGMVGTAVTVMPPQWRVSFAFIENNIIVVFENFWEGLWMNCVRQANI 60
Db 1 MATHALEIAGLFLGGVGMVGTAVTVMPPQWRVSFAFIENNIIVVFENFWEGLWMNCVRQANI 60

QY 61 RMQCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120
Db 61 RMQCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120

QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVLIIVGGA 180
Db 121 TAGIIFIITGMVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVLIIVGGA 180

QY 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV 225
Db 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV 225
```

```

; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 358
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-208-024-358

Query Match      100.0%; Score 225; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.1e-208;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATHALEIAGLFLGGVGMVGTAVTVMPPQWRVSFAFIENNIIVVFENFWEGLWMNCVRQANI 60
Db 1 MATHALEIAGLFLGGVGMVGTAVTVMPPQWRVSFAFIENNIIVVFENFWEGLWMNCVRQANI 60

QY 61 RMQCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120
Db 61 RMQCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120

QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVLIIVGGA 180
Db 121 TAGIIFIITGMVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVLIIVGGA 180

QY 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV 225
Db 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV 225

RESULT 9
US-10-201-853-358
; Sequence 358, Application US/10201853
; Publication No. US20040053358A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C465
; CURRENT APPLICATION NUMBER: US/10/201,853
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
```


Db 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNVVFENFWEGLMNCVRQANI 60
QY 61 RMQCKIYDSLALLSPDLQAARGLMCAASVMSFLAFMMAILGKCTRCTGDNEKVKAHILL 120
Db 61 RMQCKIYDSLALLSPDLQAARGLMCAASVMSFLAFMMAILGKCTRCTGDNEKVKAHILL 120
QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGA 180
Db 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGA 180
QY 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYRSQYV 225
Db 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYRSQYV 225

RESULT 11
US-10-063-512-120
; Sequence 120, Application US/10063512
; Publication No. US20030018183A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,512
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 120
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-512-120

Query Match 100.0%; Score 225; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.1e-208;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNVVFENFWEGLMNCVRQANI 60
Db 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNVVFENFWEGLMNCVRQANI 60
QY 61 RMQCKIYDSLALLSPDLQAARGLMCAASVMSFLAFMMAILGKCTRCTGDNEKVKAHILL 120
Db 61 RMQCKIYDSLALLSPDLQAARGLMCAASVMSFLAFMMAILGKCTRCTGDNEKVKAHILL 120
QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGA 180
Db 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGA 180
QY 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYRSQYV 225
Db 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYRSQYV 225

RESULT 12
US-10-063-513-120
; Sequence 120, Application US/10063513
; Publication No. US20030018172A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,513
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 120
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-513-120

Query Match 100.0%; Score 225; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.1e-208;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNVVFENFWEGLMNCVRQANI 60
Db 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNVVFENFWEGLMNCVRQANI 60
QY 61 RMQCKIYDSLALLSPDLQAARGLMCAASVMSFLAFMMAILGKCTRCTGDNEKVKAHILL 120
Db 61 RMQCKIYDSLALLSPDLQAARGLMCAASVMSFLAFMMAILGKCTRCTGDNEKVKAHILL 120
QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGA 180
Db 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGA 180
QY 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYRSQYV 225
Db 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYRSQYV 225

RESULT 13
US-10-063-515-120
; Sequence 120, Application US/10063515
; Publication No. US20030018173A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,515
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 120
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-515-120

Query Match 100.0%; Score 225; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.1e-208;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNVVFENFWEGLMNCVRQANI 60
Db 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNVVFENFWEGLMNCVRQANI 60

APPLICANT: Gurney,Austin L.
APPLICANT: Watanabe,Colin K.
APPLICANT: Wood,William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,569
CURRENT FILING DATE: 2002-05-02
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 120
LENGTH: 225
TYPE: PRT
ORGANISM: Homo Sapien
US-10-063-569-120

Query Match 100.0%; Score 225; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.1e-208;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATHALEIAGLFLGGVGMVGTVAVTVMPOWRVSFAFIENNIIVVFENFWEGLWMNCVRQANI 60
Db 1 MATHALEIAGLFLGGVGMVGTVAVTVMPOWRVSFAFIENNIIVVFENFWEGLWMNCVRQANI 60
QY 61 RMOCKIYDLSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120
Db 61 RMOCKIYDLSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120
QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIIVGGA 180
Db 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIIVGGA 180
QY 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPPSVYSRSQYV 225
Db 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPPSVYSRSQYV 225

Search completed: September 1, 2004, 17:01:06
Job time : 50 secs

QY 61 RMOCKIYDLSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120
Db 61 RMOCKIYDLSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120
QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIIVGGA 180
Db 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIIVGGA 180
QY 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPPSVYSRSQYV 225
Db 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPPSVYSRSQYV 225

RESULT 14

US-10-063-549-120
Sequence 120, Application US/10063549
Publication No. US20030027986A1
GENERAL INFORMATION:
APPLICANT: Eaton,Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney,Austin L.
APPLICANT: Watanabe,Colin K.
APPLICANT: Wood,William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,549
CURRENT FILING DATE: 2002-05-02
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 120
LENGTH: 225
TYPE: PRT
ORGANISM: Homo Sapien
US-10-063-549-120

Query Match 100.0%; Score 225; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.1e-208;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATHALEIAGLFLGGVGMVGTVAVTVMPOWRVSFAFIENNIIVVFENFWEGLWMNCVRQANI 60
Db 1 MATHALEIAGLFLGGVGMVGTVAVTVMPOWRVSFAFIENNIIVVFENFWEGLWMNCVRQANI 60
QY 61 RMOCKIYDLSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120
Db 61 RMOCKIYDLSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120
QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIIVGGA 180
Db 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIIVGGA 180
QY 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPPSVYSRSQYV 225
Db 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPPSVYSRSQYV 225

RESULT 15

US-10-063-569-120
Sequence 120, Application US/10063569
Publication No. US20030018168A1
GENERAL INFORMATION:
APPLICANT: Eaton,Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2004, 16:56:09 ; Search time 42 Seconds
(without alignments)
1690.276 Million cell updates/sec

Title: US-10-063-732-120
Perfect score: 225
Sequence: 1 MATHALEIAGLFLGGVGMVG.....QKSYHTGKKSPSVYSRSQYV 225

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 6

Total number of hits satisfying chosen parameters: 2714

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPPREMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archheap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB ID	Description
1	12	5.3	209 13 Q90XR9	Q90xr9 brachydanio
2	9	4.0	214 13 Q90XR0	Q90xr0 brachydanio
3	9	4.0	214 13 Q98SR2	Q98sr2 gallus gall
4	9	4.0	216 13 Q98SR1	Q98sr1 gallus gall
5	9	4.0	224 11 Q8BXA6	Q8bxa6 mus musculus
6	8	3.6	213 13 Q80SG0	Q80sg0 xenopus lae
7	8	3.6	214 13 Q9DE12	Q9del2 xenopus lae
8	8	3.6	214 13 Q90XQ9	Q90xq9 xenopus lae
9	8	3.6	261 2 Q9L5U5	Q9l5u5 salmonella
10	8	3.6	265 16 Q9RGT3	Q9rgt3 salmonella
11	8	3.6	311 17 Q8TQK4	Q8tgk4 methanosarc
12	8	3.6	393 16 Q89D52	Q89d52 bradyrhizob
13	8	3.6	459 16 Q81RJ5	Q8lrj5 bacillus an
14	8	3.6	460 16 Q81EE6	Q8lee6 bacillus ce
15	8	3.6	536 4 Q9HB96	Q9hb96 homo sapien
16	8	3.6	686 3 Q75013	Q75013 schizosacch

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

17	8	3.6	1419	10	Q8LQE6	Q8lqe6 oryza sativ
18	8	3.6	1607	16	Q89C03	Q89c03 bradyrhizob
19	7	3.1	22	2	Q56233	Q56233 thermus aqu
20	7	3.1	70	5	Q86KM9	Q86km9 dictyosteli
21	7	3.1	74	11	Q99KF8	Q99kf8 mus musculu
22	7	3.1	75	16	Q97FQ9	Q97fq9 clostridium
23	7	3.1	94	17	Q9HKT2	Q9hkt2 thermoplasm
24	7	3.1	133	10	Q8L8C7	Q8l8c7 ceratopteril
25	7	3.1	140	9	Q94MT4	Q94mt4 bacteriopha
26	7	3.1	143	16	Q8XH76	Q8xh76 clostridium
27	7	3.1	148	2	Q7X509	Q7x509 streptomyce
28	7	3.1	148	16	Q8YTV2	Q8ytv2 anabaena sp
29	7	3.1	148	16	Q8PDJ7	Q8pdj7 xanthomonas
30	7	3.1	156	17	Q9Y9R3	Q9y9r3 aeropyrum p
31	7	3.1	167	16	Q9Z920	Q9z920 chlamydia p
32	7	3.1	169	2	Q9AEG4	Q9aeg4 enterobacte
33	7	3.1	169	16	Q9HWS4	Q9hws4 pseudomonas
34	7	3.1	177	16	Q81UB9	Q8lub9 bacillus an
35	7	3.1	178	16	Q8UJC1	Q8ujc1 agrobacteri
36	7	3.1	182	16	Q988I5	Q988i5 rhizobium l
37	7	3.1	184	8	Q85FL1	Q85fl1 adiantum ca
38	7	3.1	185	16	Q9K235	Q9k235 chlamydia p
39	7	3.1	186	5	Q8IDK0	Q8idk0 plasmodium
40	7	3.1	192	2	Q8RJI5	Q8rji5 methylococc
41	7	3.1	198	16	Q9L180	Q9l180 streptomyce
42	7	3.1	199	4	Q7Z4Y7	Q7z4y7 homo sapien
43	7	3.1	199	13	Q7ZTS2	Q7zts2 brachydanio
44	7	3.1	206	13	Q90XS1	Q90xs1 brachydanio
45	7	3.1	210	13	Q90XR4	Q90xr4 brachydanio

ALIGNMENTS

RESULT 1

Q90XR9 ID Q90XR9 PRELIMINARY; PRT; 209 AA.

AC Q90XR9; 01-DEC-2001 (TReMBLrel. 19, Created)

DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)

DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)

DE Claudin e.

GN CLDNE.

OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI_TaxID=7955;

RN [1] SEQUENCE FROM N.A.

RP MEDLINE=21417738; PubMed=11517306;

RX Kollmar R., Nakamura S.K., Kappler J.A., Hudspeth A.J.;

RA "Expression and phylogeny of claudins in vertebrate primordia.";

RL Proc. Natl. Acad. Sci. U.S.A. 98:10196-10201(2001).

DR EMBL; AF359425; AAL01832.1; -.

DR ZFIN; ZDB-GENE-010328-5; cl dne.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0005923; C:tight junction; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR006187; Claudin.

DR InterPro; IPR005411; Claudin2.

DR InterPro; IPR006188; Claudin reg.

DR InterPro; IPR004031; PMP22_Claudin.

DR Pfam; PF00822; PMP22_Claudin; 1.

DR PRINTS; PR01077; CLAUDIN.

DR PRINTS; PR01589; CLAUDIN2.

DR PROSITE; PS01346; CLAUDIN; 1.

SQ SEQUENCE 209 AA; 22593 MW; A86F48D852E16CB2 CRC64;

Query Match 5.3%; Score 12; DB 13; Length 209;
Best Local Similarity 100.0%; Pred.No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 MOCKIYDSLAL 73
| | | | | | | | | |
Db 62 MOCKIYDSLAL 73

RESULT 2
Q90XR0 PRELIMINARY; PRT; 214 AA.
ID Q90XR0
AC Q90XR0;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE CLaudin h.
GN CLDNH.

OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21417738; PubMed=11517306;
RA Kollmar R., Nakamura S.K., Kappler J.A., Hudspeth A.J.;
RT "Expression and phylogeny of claudins in vertebrate primordia.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:10196-10201(2001).
DR EMBL; AF359434; AAL01841.1; -.
DR ZFIN; ZDB-GENE-010328-8; clnhd.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005923; C:tight junction; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR006188; Claudin reg.
DR InterPro; IPR004031; PMP22_Claudin.
DR Pfam; PF00822; PMP22_Claudin; 1.
DR PRINTS; PR01077; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN; 1.
SQ SEQUENCE 214 AA; 22788 MW; 38163AB7E50BF058 CRC64;

Query Match 4.0%; Score 9; DB 13; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 WEGLWMNCV 55
| | | | | | | | | |
Db 46 WEGLWMNCV 54

RESULT 3
Q98SR2 PRELIMINARY; PRT; 214 AA.
ID Q98SR2
AC Q98SR2;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE CLaudin-3.
GN CLDN3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Reardon E., Kojima S., Rizzolo L.J.;
RT "Sequence of chick claudin-3 cDNA.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF334677; AAK20876.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005923; C:tight junction; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR006188; Claudin reg.
DR InterPro; IPR004031; PMP22_Claudin.

DR Pfam; PF00822; PMP22_Claudin; 1.
DR PRINTS; PR01077; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN; 1.
SQ SEQUENCE 214 AA; 23090 MW; A2540116CBD53978 CRC64;

Query Match 4.0%; Score 9; DB 13; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 WEGLWMNCV 55
| | | | | | | | | |
Db 46 WEGLWMNCV 54

RESULT 4
Q98SR1 PRELIMINARY; PRT; 216 AA.
ID Q98SR1
AC Q98SR1;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE CLaudin-5.
GN CLDN5.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Reardon E., Kojima S., Rizzolo L.J.;
RT "Sequence of chick claudin-5 cDNA.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF334678; AAK20877.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005923; C:tight junction; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR006188; Claudin reg.
DR InterPro; IPR004031; PMP22_Claudin.
DR Pfam; PF00822; PMP22_Claudin; 1.
DR PRINTS; PR01077; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN; 1.
SQ SEQUENCE 216 AA; 23180 MW; 5037A882DFF5433A CRC64;

Query Match 4.0%; Score 9; DB 13; Length 216;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 WEGLWMNCV 55
| | | | | | | | | |
Db 47 WEGLWMNCV 55

RESULT 5
Q8BXA6 PRELIMINARY; PRT; 224 AA.
ID Q8BXA6
AC Q8BXA6;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Similar to claudin-17.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=22354583; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of

```
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK048287; BAC33296.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005923; C:tight junction; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR006188; Claudin reg.
DR InterPro; IPR004031; PMP22_Claudin.
DR Pfam; PF00822; PMP22_Claudin; 1.
DR PRINTS; PR01077; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN; 1.
SQ SEQUENCE 224 AA; 24653 MW; 6E049CEG3AB60A34 CRC64;

Query Match
Best Local Similarity 4.0%; Score 9; DB 11; Length 224;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 PQWRVSAFI 36
Db 28 PQWRVSAFI 36
|||||

RESULT 6
Q805G0
ID Q805G0 PRELIMINARY; PRT; 213 AA.
AC Q805G0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Claudin4L2.
GN CLDN4L2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Fujita M., Itoh M., Shibata M., Taira S., Taira M.;
RT "Gene expression pattern analysis of the tight junction protein,
RT Claudin, in the early morphogenesis of Xenopus embryos.";
RL Gene Expr. Patterns 2:23-26 (2002).
DR EMBL; AB072909; BAC21014.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005923; C:tight junction; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR006188; Claudin reg.
DR InterPro; IPR004031; PMP22_Claudin.
DR Pfam; PF00822; PMP22_Claudin; 1.
DR PRINTS; PR01077; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN; 1.
SQ SEQUENCE 213 AA; 22913 MW; ACF10FC95F9C16A1 CRC64;

Query Match
Best Local Similarity 3.6%; Score 8; DB 13; Length 213;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 WEGLWMNC 54
Db 47 WEGLWMNC 54
|||||

RESULT 7
Q9DE12
ID Q9DE12 PRELIMINARY; PRT; 214 AA.
AC Q9DE12;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Transmembrane tight junction protein claudin.
GN CLA.
```

```
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Dorsal lip;
RX MEDLINE=21098758; PubMed=11161574;
RA Brizuela B.J., Wessely O., De Robertis E.M.;
RT "Overexpression of the Xenopus Tight-Junction Protein Claudin Causes
RT Randomization of the Left-Right Body Axis.";
RL Dev. Biol. 230:217-229 (2001).
DR EMBL; AF224712; AAG44257.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005923; C:tight junction; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR006188; Claudin reg.
DR InterPro; IPR004031; PMP22_Claudin.
DR Pfam; PF00822; PMP22_Claudin; 1.
DR PRINTS; PR01077; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN; 1.
SQ SEQUENCE 214 AA; 23151 MW; 3F0D65E3ADE311E6 CRC64;

Query Match
Best Local Similarity 3.6%; Score 8; DB 13; Length 214;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 WEGLWMNC 54
Db 47 WEGLWMNC 54
|||||

RESULT 8
Q90XQ9
ID Q90XQ9 PRELIMINARY; PRT; 214 AA.
AC Q90XQ9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Claudin A (Claudin4L1).
GN CLDNA OR CLDN4L1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21417738; PubMed=11517306;
RA Kollmar R., Nakamura S.K., Kappler J.A., Hudspeth A.J.;
RT "Expression and phylogeny of claudins in vertebrate primordia.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:10196-10201 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Fujita M., Itoh M., Shibata M., Taira S., Taira M.;
RT "Gene expression pattern analysis of the tight junction protein,
RT Claudin, in the early morphogenesis of Xenopus embryos.";
RL Gene Expr. Patterns 2:23-26 (2002).
DR EMBL; AF359435; AAL01842.1; -.
DR EMBL; AB072908; BAC21013.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005923; C:tight junction; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR006188; Claudin reg.
DR InterPro; IPR004031; PMP22_Claudin.
DR Pfam; PF00822; PMP22_Claudin; 1.
DR PRINTS; PR01077; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN; 1.
SQ SEQUENCE 214 AA; 22952 MW; 8E86F0EB2B72357D CRC64;
```


Query Match 3.6%; Score 8; DB 13; Length 214;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 WEGLWMNC 54
Db 47 WEGLWMNC 54

RESULT 9

Q9L5U5 PRELIMINARY; PRT; 261 AA.
AC Q9L5U5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Orf, hypothetical protein.
GN TRHE.
OS Salmonella typhi.
OG Plasmid R27.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]

RP SEQUENCE FROM N.A. PubMed=10773089;
RX MEDLINE=20280091; Gilmour M.W., Blattner F.R., Burland V.,
RA Sherburne C.K., Lawley T.D., Gilmour M.W., Blattner F.R., Burland V.,
RA Grobeck E., Rose D.J., Taylor D.E.;
RT "The complete DNA sequence and analysis of R27, a large IncHI plasmid
RT from Salmonella typhi that is temperature sensitive for transfer.";
RL Nucleic Acids Res. 28:2177-2186(2000).
DR EMBL; AF250878; AAF69870.1; --
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 261 AA; 29233 MW; C1B12E63D3C86C16 CRC64;

Query Match 3.6%; Score 8; DB 2; Length 261;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 ALSPDLQA 79
Db 146 ALSPDLQA 153

RESULT 10

Q9RGT3 PRELIMINARY; PRT; 265 AA.
ID Q9RGT3
AC Q9RGT3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE TrHE (Putative pilus assembly protein).
GN TRHE OR HCM1.70.
OS Salmonella typhi.
OG Plasmid R27, and Plasmid pHCM1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC PLASMID=R27;
RX MEDLINE=99296679; PubMed=10366528;
RA Rucker M.M., Sherburne C., Lawley T.D., Taylor D.E.;
RT "Characterization of the Tra2 region of the IncHI1 plasmid R27.";
RL Plasmid 41:226-239(1999).
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN=CT18; PLASMID=pHCM1;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,

RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
DR EMBL; AF105019; AAD54051.1; --
DR EMBL; AL513383; CAD09678.1; --
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid; Complete proteome.
SQ SEQUENCE 265 AA; 29763 MW; AE66D5B0C9ECF9C7 CRC64;

Query Match 3.6%; Score 8; DB 16; Length 265;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 ALSPDLQA 79
Db 150 ALSPDLQA 157

RESULT 11

Q8TQK4 PRELIMINARY; PRT; 311 AA.
ID Q8TQK4
AC Q8TQK4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein MA1538.
GN MA1538.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam I.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity.";
RL Genome Res. 12:532-542(2002).
DR EMBL; AE010823; AAM04952.1; --
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 311 AA; 34303 MW; 41E4060862A4E410 CRC64;

Query Match 3.6%; Score 8; DB 17; Length 311;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 DSLLALSP 75
Db 230 DSLLALSP 237

RESULT 12

Q89D52 PRELIMINARY; PRT; 393 AA.
ID Q89D52
AC Q89D52;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	
DE	Multidrug resistance efflux pump.	
GN	BLR7593.	
OS	Bradyrhizobium japonicum.	
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;	
OC	Bradyrhizobiaceae; Bradyrhizobium.	
OX	NCBI_TaxID=375;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=USDA 110;	
RX	MEDLINE=22484998; PubMed=12597275;	
RA	Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,	
RA	Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,	
RA	Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,	
RA	Tabata S.;	
RT	"Complete genomic sequence of nitrogen-fixing symbiotic bacterium	
RT	Bradyrhizobium japonicum USDA110.";	
RL	DNA Res. 9:189-197(2002).	
DR	EMBL; AP005962; BAC52858.1; -.	
DR	GO; GO:0016020; C:membrane; IEA.	
DR	GO; GO:0015428; F:type I protein secretor activity; IEA.	
DR	GO; GO:0009306; P:protein secretion; IEA.	
DR	InterPro; IPR006143; HlyD.	
DR	InterPro; IPR003997; RtxD.	
DR	Pfam; PF00529; HlyD; 1.	
DR	PRINTS; PR01490; RTXTOXIND.	
KW	Complete proteome.	
SQ	SEQUENCE 393 AA; 42533 MW; E40240F53E0D44E2 CRC64;	
Query Match		
Best Local Similarity 3.6%; Score 8; DB 16; Length 393;		
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	109 GDNEKVKA 116	
Db		
	92 GDNEKVKA 99	
RESULT 13		
Q81RJ5		
ID	Q81RJ5	PRELIMINARY; PRT; 459 AA.
AC	Q81RJ5;	
DT	01-JUN-2003 (TrEMBLrel. 24, Created)	
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)	
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	
DE	Polysaccharide biosynthesis family protein.	
GN	BA2049.	
OS	Bacillus anthracis (strain Ames).	
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	
OX	NCBI_TaxID=198094;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=22608414; PubMed=12721629;	
RA	Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,	
RA	Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,	
RA	Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,	
RA	Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,	
RA	DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,	
RA	Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,	
RA	Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,	
RA	Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,	
RA	Hazen A., Cline R., Redmond C., Thwaites J.E., White O., Salzberg S.L.,	
RA	Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,	
RA	Fraser C.M.;	
RT	"The genome sequence of Bacillus anthracis Ames and comparison to	
RT	closely related bacteria.";	
RL	Nature 423:81-86(2003).	
DR	EMBL; AE017030; AAP25937.1; -.	
DR	TIGR; BA2049; -.	
DR	GO; GO:0016020; C:membrane; IEA.	
DR	GO; GO:0003676; F:nucleic acid binding; IEA.	
DR	GO; GO:0000271; P:polysaccharide biosynthesis; IEA.	
DR	InterPro; IPR002797; Polysacc_synt.	
DR	InterPro; IPR000504; RNA_rec_mot.	
DR	Pfam; PF01943; Polysacc_synt; 1.	
DR	PROSITE; PS00030; RRM_RNP_1; 1.	
KW	Complete proteome.	
SQ	SEQUENCE 460 AA; 50684 MW; 8A5568EC9EB045E5 CRC64;	
Query Match		
Best Local Similarity 3.6%; Score 8; DB 16; Length 460;		
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	131 MVVLIPVS 138	
Db		
	298 MVVLIPVS 305	
RESULT 15		
Q9HB96		
ID	Q9HB96	PRELIMINARY; PRT; 536 AA.
AC	Q9HB96;	
DT	01-MAR-2001 (TrEMBLrel. 16, Created)	
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)	
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	
DE	Fanconi anemia protein E (Fanconi anemia, complementation group E)	
DE	(DJ109F14.5).	
GN	FANCE.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
DR	InterPro; IPR000504; RNA_rec_mot.	
DR	Pfam; PF01943; Polysacc_synt; 1.	
DR	PROSITE; PS00030; RRM_RNP_1; 1.	
KW	Complete proteome.	
SQ	SEQUENCE 459 AA; 50450 MW; 8FECC87C3E51CBAB CRC64;	
Query Match		
Best Local Similarity 3.6%; Score 8; DB 16; Length 459;		
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	131 MVVLIPVS 138	
Db		
	297 MVVLIPVS 304	
RESULT 14		
Q81EE6		
ID	Q81EE6	PRELIMINARY; PRT; 460 AA.
AC	Q81EE6;	
DT	01-JUN-2003 (TrEMBLrel. 24, Created)	
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)	
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	
DE	Export protein for polysaccharides and teichoic acids.	
GN	BC2034.	
OS	Bacillus cereus (strain ATCC 14579 / DSM 31).	
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	
OX	NCBI_TaxID=226900;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=22608415; PubMed=12721630;	
RA	Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,	
RA	Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,	
RA	Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,	
RA	Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,	
RA	Overbeek R., Kyrpides N.;	
RT	"Genome sequence of Bacillus cereus and comparative analysis with	
RT	Bacillus anthracis.";	
RL	Nature 423:87-91(2003).	
DR	EMBL; AE017004; AAP09003.1; -.	
DR	GO; GO:0016020; C:membrane; IEA.	
DR	GO; GO:0003676; F:nucleic acid binding; IEA.	
DR	GO; GO:0000271; P:polysaccharide biosynthesis; IEA.	
DR	InterPro; IPR002797; Polysacc_synt.	
DR	InterPro; IPR000504; RNA_rec_mot.	
DR	Pfam; PF01943; Polysacc_synt; 1.	
DR	PROSITE; PS00030; RRM_RNP_1; 1.	
KW	Complete proteome.	
SQ	SEQUENCE 460 AA; 50684 MW; 8A5568EC9EB045E5 CRC64;	

RP SEQUENCE FROM N.A.
RX MEDLINE=20489873; PubMed=11001585;
RA de Winter J.P., Leveille F., van Berkel C.G.M., Rooimans M.A.,
RA van der Weel L., Steltenpool J., Demuth I., Morgan N.V., Alon N.,
RA Bosnoyan-Collins L., Lightfoot J., Leegwater P.A., Waisfisz Q.,
RA Komatsu K., Arwert F., Pronk J.C., Mathew C.G., Digweed M.,
RA Buchwald M., Joenje H.;
RT "Isolation of a cDNA representing the Fanconi anemia complementation
RT group E gene.";
RL Am. J. Hum. Genet. 67:1306-1308 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Phillips S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF265210; AAG16743.1; -.
DR EMBL; BC046359; AAH46359.1; -.
DR EMBL; AL022721; CAD92504.1; -.
DR Genew; HGNC:3586; FANCE.
DR GO; GO:0005634; C:nucleus; NAS.
SQ SEQUENCE 536 AA; 58710 MW; 0E94D8C469C791A5 CRC64;

Query Match 3.6%; Score 8; DB 4; Length 536;
Best Local Similarity 100.0%; Pred.No. 37;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 LLALSPDL 77
Db 348 LLALSPDL 355

Search completed: September 1, 2004, 16:59:28
Job time : 46 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2004, 16:56:30 ; Search time 16 Seconds
(without alignments)
1352.693 Million cell updates/sec

Title: US-10-063-732-120
Perfect score: 225
Sequence: 1 MATHALEIAGLFLGGVMVG.....QKSYHTGKKSPSVYRSQYV 225

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 6

Total number of hits satisfying chosen parameters: 1068

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	9	4.0	280	2	A39484	androgen-withdrawa
2	8	3.6	686	2	T39650	probable multifunc
3	7	3.1	22	2	T45268	hypothetical prote
4	7	3.1	75	2	D97228	hypothetical prote
5	7	3.1	115	2	T11448	NADH2 dehydrogenas
6	7	3.1	115	2	G69811	hypothetical prote
7	7	3.1	148	2	AD2132	hypothetical prote
8	7	3.1	156	2	E72531	hypothetical prote
9	7	3.1	167	2	B72112	hypothetical prote
10	7	3.1	167	2	D86511	hypothetical prote
11	7	3.1	169	2	A83134	conserved hypothet
12	7	3.1	178	2	AH2577	conserved hypothet
13	7	3.1	178	2	G97359	fxsa protein (VC26
14	7	3.1	185	2	E81559	hypothetical prote
15	7	3.1	213	2	C83772	hypothetical prote
16	7	3.1	215	2	A56168	deoxyadenosine kin
17	7	3.1	238	2	B89789	conserved hypothet
18	7	3.1	248	2	AC1919	hypothetical prote
19	7	3.1	253	2	S20738	chitinase (EC 3.2.
20	7	3.1	253	2	B34801	pathogenesis-relat
21	7	3.1	274	2	E83423	conserved hypothet
22	7	3.1	287	2	S74944	hypothetical prote
23	7	3.1	295	2	B69653	transmembrane lipo
24	7	3.1	330	2	AD2130	transcription regu
25	7	3.1	351	1	S76613	N-acetyl-gamma-glu
26	7	3.1	352	2	AB2248	N-acetyl-glutamate
27	7	3.1	382	2	AF2994	glycosyltransferas
28	7	3.1	382	2	D98289	hypothetical prote
29	7	3.1	399	2	F83094	cell division prot

30	7	3.1	407	2	AE0121	probable membrane
31	7	3.1	427	2	E83530	hypothetical prote
32	7	3.1	442	2	T16773	hypothetical prote
33	7	3.1	443	2	D82975	two-component sens
34	7	3.1	450	2	AI0909	probable membrane
35	7	3.1	451	2	S77599	probable coproporp
36	7	3.1	459	2	G82431	C4-dicarboxylate t
37	7	3.1	463	2	E81141	xanthine/uracil pe
38	7	3.1	465	2	T16835	hypothetical prote
39	7	3.1	480	2	E72682	conserved hypothet
40	7	3.1	482	2	B70205	probable arop2 pro
41	7	3.1	487	2	C70574	glutamine syntheta
42	7	3.1	491	2	E69368	probable sugar tra
43	7	3.1	499	2	AF0117	sodium/proton anti
44	7	3.1	500	2	F83418	CaLB protein - Ara
45	7	3.1	510	2	T50526	

ALIGNMENTS

RESULT 1
A39484

androgen-withdrawal apoptosis protein RVp1, prostatic - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 04-Mar-2000

C;Accession: A39484

R;Briehl, M.M.; Miesfeld, R.L.

Mol. Endocrinol. 5, 1381-1388, 1991

A;Title: Isolation and characterization of transcripts induced by androgen withdrawal a

A;Reference number: A39484; MUID:92130987; PMID:1723140

A;Accession: A39484

A;Molecule type: mRNA

A;Residues: 1-280 <BRI>

A;Cross-references: GB:M74067; NID:g205857; PIDN:AAA41760.1; PID:g205858

C;Genetics:

A;Gene: RVp.1

C;Superfamily: rat androgen-withdrawal apoptosis protein RVp1

Query Match 4.0%; Score 9; DB 2; Length 280;
Best local Similarity 100.0%; Pred. No. 0.58;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 WEGLWMNCV 55

Db 46 WEGLWMNCV 54

RESULT 2

T39650

probable multifunctional folic acid synthesis protein - fission yeast (Schizosaccharomyc

N;Alternate names: dihydropterate synthase

N;Contains: dihydroneopterin aldolase (EC 4.1.2.25); dihydropteroate synthase (EC 2.5.1

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Sep-2000

C;Accession: T39650; T40272

R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.

submitted to the EMBL Data Library, October 1998

A;Reference number: Z21868

A;Accession: T39650

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-686 <LYN>

A;Cross-references: EMBL:AL031856; PIDN:CAA21297.1; GSPDB:GN00067; SPDB:SPBC1734.03

A;Experimental source: strain 972h-; cosmid c1734

A;Accession: T40272

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-686 <LY2>

A;Cross-references: EMBL:AL031854; PIDN:CAA21289.1; GSPDB:GN00067; SPDB:SPBC337.19

A;Experimental source: strain 972h-; cosmid c337

C;Genetics:

A;Gene: SPBC1734.03; SPBC337.19

A;Map position: 2
C;Superfamily: fasB-fasC-fasD multifunctional enzyme; 2-amino-4-hydroxy-6-hydroxymethyl
G
C;Keywords: aldehyde-lyase; carbon-carbon lyase; transferase
F;6-122/Domain: dihydroneopterin aldolase homology <DHA1>
F;130-232/Domain: dihydroneopterin aldolase homology <DHA2>
F;253-385/Domain: 2-amino-4-hydroxy-6-hydroxymethyl dihydropteridine pyrophosphokinase ho
Query Match 3.6%; Score 8; DB 2; Length 686;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 70 LLALSPDL 77
| | | | | | | |
Db 375 LLALSPDL 382
RESULT 3
T45268
hypothetical protein [imported] - Thermus aquaticus
C;Species: Thermus aquaticus
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 31-Jan-2000
C;Accession: T45268
R;Motoshima, H.; Minagawa, E.; Tsukasaki, F.; Kaminogawa, S.
J. Ferment. Bioeng. 86, 21-27, 1998
A;Title: Cloning and nucleotide sequencing of genes encoding Mn-superoxide dismutase and
A;Reference number: Z22952
A;Accession: T45268
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-22 <MOT>
A;Cross-references: EMBL:D84646; PIDN:BAAL2701.1
A;Experimental source: strain YT-1

Query Match 3.1%; Score 7; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 172 ALVLIVG 178
| | | | | | | |
Db 10 ALVLIVG 16
RESULT 4
D97228
hypothetical protein CAC2668 [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: D97228
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: D97228
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-75 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK80615.1; PID:g15025698; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC2668

Query Match 3.1%; Score 7; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 ALEIAGL 11
| | | | | | | |
Db 4 ALEIAGL 10

RESULT 5

T11448
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - nine-banded armadillo mitochondr
C;Species: mitochondrion Dasypus novemcinctus (nine-banded armadillo)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
C;Accession: T11448
R;Arnason, U.; Gullberg, A.; Janke, A.
Mol. Biol. Evol. 14, 762-768, 1997
A;Title: Phylogenetic analysis of mitochondrial DNA suggest a sister group relationship
A;Reference number: Z17272; MUID:97357423; PMID:9214749
A;Accession: T11448
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-115 <ARN>
A;Cross-references: EMBL:Y11832; NID:g2252500; PIDN:CAA72523.1; PID:g2252508
C;Genetics:
A;Gene: NADH3
A;Genome: mitochondrion
A;Genetic code: SGCI
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 3
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 3.1%; Score 7; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 170 TTALVLI 176
| | | | | | | |
Db 89 TTALVLI 95

RESULT 6
G69811
hypothetical protein yflt - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C;Accession: G69811
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelli
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: G69811
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-115 <KUN>
A;Cross-references: GB:Z99108; GB:AL009126; NID:g2633055; PIDN:CAB12584.1; PID:g2633079
A;Experimental source: strain 168
C;Genetics:
A;Gene: yflt
C;Superfamily: Bacillus subtilis hypothetical protein yflt

Query Match 3.1%; Score 7; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 110 DNEKVKA 116
| | | | | | | |
Db 107 DNEKVKA 113

RESULT 7
AD2132


```
hypothetical protein all2611 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AD2132
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AD2132
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-148 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB74310.1; PID:g17131704; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all2611

Query Match          3.1%; Score 7; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 ALSPDLQ 78
|||||
Db 51 ALSPDLQ 57

RESULT 8
E72531
hypothetical protein APE2225 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: E72531
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: E72531
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-156 <KAW>
A;Cross-references: DDBJ:AP000063; NID:g5105654; PIDN:BAA81237.1; PID:d1045023; PID:g510
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE2225

Query Match          3.1%; Score 7; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 KRELGEA 164
|||||
Db 150 KRELGEA 156

RESULT 9
B72112
hypothetical protein - Chlamydophila pneumoniae (strain CWL029)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
C;Accession: B72112
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
A;Accession: B72112
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-167 <ARN>
A;Cross-references: GB:AE001603; GB:AE001363; NID:g4376422; PIDN:AAD18317.1; PID:g437643
A;Experimental source: strain CWL029
```

```
C;Genetics:
A;Gene: CPn0164

Query Match          3.1%; Score 7; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 LIVGGAL 181
|||||
Db 47 LIVGGAL 53

RESULT 10
D86511
hypothetical protein CPj0164 [imported] - Chlamydophila pneumoniae (strain J138)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C;Accession: D86511
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: D86511
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-167 <STO>
A;Cross-references: GB:BA000008; NID:g8978537; PIDN:BAA98374.1; GSPDB:GN00142
A;Experimental source: strain J138
C;Genetics:
A;Gene: CPj0164

Query Match          3.1%; Score 7; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 LIVGGAL 181
|||||
Db 47 LIVGGAL 53

RESULT 11
A83134
conserved hypothetical protein PA4104 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: A83134
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83134
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-169 <STO>
A;Cross-references: GB:AE004826; GB:AE004091; NID:g9950296; PIDN:AAG07491.1; GSPDB:GN001
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA4104

Query Match          3.1%; Score 7; DB 2; Length 169;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 TALVLIV 177
|||||
Db 93 TALVLIV 99

RESULT 12
AH2577
conserved hypothetical protein fxsA [imported] - Agrobacterium tumefaciens (strain C58, ;
```

C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AH2577
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AH2577
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-178 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL41038.1; PID:g17738323; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: fxsA
A;Map position: circular chromosome
C;Superfamily: Escherichia coli hypothetical protein b4140

Query Match 3.1%; Score 7; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 LGGVGMV 19
|||||
Db 50 LGGVGMV 56

RESULT 13

G97359
fxsA protein (VC2696) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: G97359
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: G97359
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-178 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK85832.1; PID:g15154865; GSPDB:GN00169
C;Genetics:
A;Gene: AGR_C_11
A;Map position: circular chromosome
C;Superfamily: Escherichia coli hypothetical protein b4140

Query Match 3.1%; Score 7; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 LGGVGMV 19
|||||
Db 50 LGGVGMV 56

RESULT 14

E81559
hypothetical protein CP0607 [imported] - Chlamydophila pneumoniae (strain AR39)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
C;Accession: E81559
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: E81559

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-185 <REA>
A;Cross-references: GB:AE002218; GB:AE002161; NID:g7189509; PIDN:AAF38423.1; PID:g718951
A;Experimental source: strain AR39, HL cells
C;Genetics:
A;Gene: CP0607

Query Match 3.1%; Score 7; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 LIVG GAL 181
|||||
Db 65 LIVG GAL 71

RESULT 15

C83772
hypothetical protein BH0979 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: C83772
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: C83772

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-213 <STO>
A;Cross-references: GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BAB04698.1; GSPDB:GN00
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH0979

Query Match 3.1%; Score 7; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 ILLTAGI 124
|||||
Db 73 ILLTAGI 79

Search completed: September 1, 2004, 16:59:49
Job time : 20 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2004, 16:55:44 ; Search time 12 Seconds
(without alignments)
976.315 Million cell updates/sec

Title: US-10-063-732-120
Perfect score: 225
Sequence: 1 MATHALEIAGLFLGGVMVG.....QKSYHTGKKSPTSVSRSQYV 225

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 6

Total number of hits satisfying chosen parameters: 608

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	225	100.0	225	1	CLD8_HUMAN	P56748 homo sapien
2	13	5.8	225	1	CLD8_MOUSE	Q9z260 mus musculu
3	10	4.4	208	1	CLDY_BRARE	Q9yh91 brachydanio
4	9	4.0	209	1	CLD4_CERAE	019005 cercopithec
5	9	4.0	209	1	CLD4_HUMAN	014493 homo sapien
6	9	4.0	210	1	CLD4_MOUSE	035054 mus musculu
7	9	4.0	218	1	CLD3_CANFA	Q95km5 canis famil
8	9	4.0	219	1	CLD3_MOUSE	Q9z0g9 mus musculu
9	9	4.0	219	1	CLD3_RAT	Q63400 rattus norv
10	9	4.0	220	1	CLD3_HUMAN	015551 homo sapien
11	8	3.6	224	1	CLDH_HUMAN	P56750 homo sapien
12	7	3.1	115	1	GL7M_BACSU	P80241 bacillus su
13	7	3.1	115	1	NU3M_DASNO	021332 dasypus nov
14	7	3.1	191	1	CLD7_RAT	Q9z111 rattus norv
15	7	3.1	209	1	CLDZ_BRARE	Q9yh90 brachydanio
16	7	3.1	211	1	CLD7_HUMAN	Q95471 homo sapien
17	7	3.1	211	1	CLDJ_MOUSE	Q9z261 mus musculu
18	7	3.1	211	1	CLDJ_HUMAN	Q8n6f1 homo sapien
19	7	3.1	211	1	CLDJ_MOUSE	Q9et38 mus musculu
20	7	3.1	214	1	DGK1_LACAC	Q59483 lactobacill
21	7	3.1	215	1	CLDX_BRARE	Q9yh92 brachydanio
22	7	3.1	217	1	CLD9_HUMAN	Q95484 homo sapien
23	7	3.1	217	1	CLD9_MOUSE	Q9z057 mus musculu
24	7	3.1	219	1	CLD6_MOUSE	Q9z262 mus musculu
25	7	3.1	220	1	CLD6_HUMAN	P56747 homo sapien
26	7	3.1	230	1	CLD2_HUMAN	Q95km6 canis famil
27	7	3.1	230	1	CLD2_MOUSE	P57739 homo sapien
28	7	3.1	230	1	CLD2_MOUSE	Q88552 mus musculu
29	7	3.1	239	1	CLDE_HUMAN	Q95500 homo sapien
30	7	3.1	239	1	CLDE_MOUSE	Q9z0s3 mus musculu
31	7	3.1	253	1	CHIQ_TOBAC	P17514 nicotiana t
32	7	3.1	274	1	NAGB_FUSNN	Q8reg1 fusobacteri
33	7	3.1	278	1	KSGA_METKA	Q8twu7 methanopyru

34	7	3.1	287	1	BTPA_SYNY3	P72966 synechocyst
35	7	3.1	295	1	LPLC_BACSU	P39129 bacillus su
36	7	3.1	312	1	XERC_RHILO	Q98ed9 rhizobium l
37	7	3.1	351	1	ARGC_SYNY3	P54899 synechocyst
38	7	3.1	352	1	ARC1_ANASP	Q8yrb1 anabaena sp
39	7	3.1	352	1	ARGC_NOSEL	O87890 nostoc elli
40	7	3.1	354	1	VATC_HORVU	Q9scb9 hordeum vul
41	7	3.1	443	1	PHOR_PSEAE	P23621 pseudomonas
42	7	3.1	451	1	HEMN_PARDE	Q51676 paracoccus
43	7	3.1	459	1	DCUC_VIBCH	Q9kl56 vibrio chol
44	7	3.1	487	1	Y346_MYCTU	O06297 mycobacteri
45	7	3.1	491	1	GLNA_ARCFU	O29313 archaeoglob

ALIGNMENTS

RESULT 1
CLD8_HUMAN
ID CLD8_HUMAN STANDARD; PRT; 225 AA.
AC P56748;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Claudin-8.
GN CLDN8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Keen T.J., Inglehearn C.F.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20289799; PubMed=10830953;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
RA Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
RA Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
RA Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
RA Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA Lehrach H., Reinhardt R., Yaspo M.-L.;
RT "The DNA sequence of human chromosome 21.";
RL Nature 405:311-319 (2000).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

CC -!- FUNCTION: Component of tight junction (TJ) strands.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: Belongs to the claudin family.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; AJ250711; CAB60615.1; -.

CC EMBL; AP001707; BAA95567.1; -.

CC EMBL; BC020866; AAH20866.1; -.

CC EMBL; BC058004; AAH58004.1; -.

CC Genew; HGNC:2050; CLDN8.

CC InterPro; IPR006187; Claudin.

CC InterPro; IPR006188; Claudin reg.

CC InterPro; IPR004031; PMP22_Claudin.

CC Pfam; PF00822; PMP22_Claudin; 1.

CC PRINTS; PR01077; CLAUDIN.

CC PROSITE; PS01346; CLAUDIN; 1.

CC Tight junction; Transmembrane.

CC TRANSMEM 8 28 POTENTIAL.

CC TRANSMEM 82 102 POTENTIAL.

CC TRANSMEM 118 138 POTENTIAL.

CC TRANSMEM 167 187 POTENTIAL.

CC SEQUENCE 225 AA; 24845 MW; F7920E8E71682473 CRC64;

Query Match 100.0%; Score 225; DB 1; Length 225;

Best Local Similarity 100.0%; Pred. No. 4.4e-226;

Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATHALEIAGLFLGGVGMVGTAVTVMPQWRVSFAFENNIVVFENFWEGLMNCVRQANI 60

Db 1 MATHALEIAGLFLGGVGMVGTAVTVMPQWRVSFAFENNIVVFENFWEGLMNCVRQANI 60

QY 61 RMQCKIYDSLALLSPDLQAAGLMCAASVMSFLAFMMAILGKCTRCTGDNEKVKAHILL 120

Db 61 RMQCKIYDSLALLSPDLQAAGLMCAASVMSFLAFMMAILGKCTRCTGDNEKVKAHILL 120

QY 121 TAGIIFIITGMVLLIPVSWVANAIIRDFFNSIVNVAQKRELGEALYLGWTTALVLIVGGA 180

Db 121 TAGIIFIITGMVLLIPVSWVANAIIRDFFNSIVNVAQKRELGEALYLGWTTALVLIVGGA 180

QY 181 LFCCVFCCKEKKSSSYRISIPSHRTTQKSYHTGKSPSVYSRQYV 225

Db 181 LFCCVFCCKEKKSSSYRISIPSHRTTQKSYHTGKSPSVYSRQYV 225

RESULT 2

CLD8_MOUSE

ID CLD8_MOUSE STANDARD; PRT; 225 AA.

AC Q9Z260;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Claudin-8.

GN CLDN8.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A. PubMed=9892664;

RX MEDLINE=99110921; Fujimoto K., Tsukita S.;

RA Morita K., Furuse M., Fujimoto K., Tsukita S.;

RT "Claudin multigene family encoding four-transmembrane domain protein

RT components of tight junction strands.";

RL Proc. Natl. Acad. Sci. U.S.A. 96:511-516 (1999).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Breast tumor;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,

RA Blakesley R.W., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

CC -!- FUNCTION: Component of tight junction (TJ) strands.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: Belongs to the claudin family.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; AF087826; AAD09761.1; -.

CC EMBL; BC003868; AAH03868.1; -.

CC MGD; MGI:1859286; Cldn8.

CC InterPro; IPR006187; Claudin.

CC InterPro; IPR006188; Claudin reg.

CC InterPro; IPR004031; PMP22_Claudin.

CC Pfam; PF00822; PMP22_Claudin; 1.

CC PRINTS; PR01077; CLAUDIN.

CC PROSITE; PS01346; CLAUDIN; 1.

CC Tight junction; Transmembrane.

CC TRANSMEM 8 28 POTENTIAL.

CC TRANSMEM 82 102 POTENTIAL.

CC TRANSMEM 118 138 POTENTIAL.

CC TRANSMEM 167 187 POTENTIAL.

CC SEQUENCE 225 AA; 24947 MW; 12BB3C460F23D876 CRC64;

Query Match 5.8%; Score 13; DB 1; Length 225;

Best Local Similarity 100.0%; Pred. No. 1e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 LGGVGMVGTAVT 25

Db 13 LGGVGMVGTAVT 25

RESULT 3

CLDY_BRARE

ID CLDY_BRARE STANDARD; PRT; 208 AA.

AC Q9YH91;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Claudin-like protein ZF-A89.

OS Brachydanio rerio (Zebrafish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

```
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Keen T.J., Inglehearn C.F.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Component of tight junction (TJ) strands.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the claudin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ011789; CAA09777.1; -.
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR005411; Claudin2.
DR InterPro; IPR006188; Claudin reg.
DR InterPro; IPR004031; PMP22_Claudin.
DR Pfam; PF00822; PMP22_Claudin; 1.
DR PRINTS; PR01077; CLAUDIN.
DR PRINTS; PR01589; CLAUDIN2.
DR PROSITE; PS01346; CLAUDIN; 1.
KW Tight junction; Transmembrane.
FT TRANSMEM 8 28 POTENTIAL.
FT TRANSMEM 82 102 POTENTIAL.
FT TRANSMEM 117 137 POTENTIAL.
FT TRANSMEM 160 180 POTENTIAL.
SQ SEQUENCE 208 AA; 22205 MW; 6A4BB5EBF3CCAB81 CRC64;

Query Match 4.4%; Score 10; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 FWEGLWMNCV 55
Db 46 FWEGLWMNCV 55

RESULT 4
CLD4_CERAE STANDARD; PRT; 209 AA.
AC O19005;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Claudin-4 (Clostridium perfringens enterotoxin receptor) (CPE-
DE receptor) (CPE-R).
GN CLDN4 OR CPETR1 OR CPER.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97242441; PubMed=9087440;
RA Katahira J., Inoue N., Horiguchi Y., Matsuda M., Sugimoto N.;
RT "Molecular cloning and functional characterization of the receptor for
RT Clostridium perfringens enterotoxin.";
RL J. Cell Biol. 136:1239-1247(1997).
CC -!- FUNCTION: Component of tight junction (TJ) strands.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the claudin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
```

```
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D88492; BAA22781.1; -.
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR006188; Claudin reg.
DR InterPro; IPR004031; PMP22_Claudin.
DR Pfam; PF00822; PMP22_Claudin; 1.
DR PRINTS; PR01077; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN; 1.
KW Tight junction; Transmembrane.
FT TRANSMEM 10 30 POTENTIAL.
FT TRANSMEM 82 102 POTENTIAL.
FT TRANSMEM 118 138 POTENTIAL.
FT TRANSMEM 161 181 POTENTIAL.
SQ SEQUENCE 209 AA; 22029 MW; 474DB3099F95289E CRC64;

Query Match 4.0%; Score 9; DB 1; Length 209;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 WEGLWMNCV 55
Db 47 WEGLWMNCV 55

RESULT 5
CLD4_HUMAN STANDARD; PRT; 209 AA.
ID CLD4_HUMAN
AC O14493;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Claudin-4 (Clostridium perfringens enterotoxin receptor) (CPE-
DE receptor) (CPE-R) (Williams-Beuren syndrome chromosome region 8
DE protein).
GN CLDN4 OR CPETR1 OR CPER OR WBSR8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=97476271; PubMed=9334247;
RA Katahira J., Sugiyama H., Inoue N., Horiguchi Y., Matsuda M.,
RA Sugimoto N.;
RT "Clostridium perfringens enterotoxin utilizes two structurally related
RT membrane proteins as functional receptors in vivo.";
RL J. Biol. Chem. 272:26652-26658(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
```


RT "Claudin multigene family encoding four-transmembrane domain protein components of tight junction strands.";
RT Proc. Natl. Acad. Sci. U.S.A. 96:511-516(1999).
RL -!- FUNCTION: Component of tight junction (TJ) strands.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the claudin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC
CC EMBL; AB000713; BAA22985.1; -.
DR EMBL; AF087822; AAD09757.1; -.
DR MGD; MGI:131314; Cldn4.
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR006188; Claudin reg.
DR InterPro; IPR004031; PMP22 Claudin.
DR Pfam; PF00822; PMP22 Claudin; 1.
DR PRINTS; PR01077; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN; 1.
KW Tight junction; Transmembrane.
FT TRANSMEM 8 28 POTENTIAL.
FT TRANSMEM 82 102 POTENTIAL.
FT TRANSMEM 117 137 POTENTIAL.
FT TRANSMEM 161 181 POTENTIAL.
FT SEQUENCE 210 AA; 22338 MW; 3B6D571EC71D6564 CRC64;
SQ

Query Match 4.0%; Score 9; DB 1; Length 210;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 WEGLWMNCV 55
Db 47 WEGLWMNCV 55
|||||

RESULT 7
CLD3_CANFA STANDARD; PRT; 218 AA.
ID CLD3_CANFA STANDARD; PRT; 218 AA.
AC Q95KM5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Claudin-3.
GN CLDN3.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Carnivora; Fissipedia; Canidae; Canis.
OC NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=21206012; PubMed=11309408;
RA Furuse M., Furuse K., Sasaki H., Tsukita S.;
RT "Conversion of zonulae occludentes from tight to leaky strand type by introducing claudin-2 into Madin-Darby canine kidney I cells.";
RL J. Cell Biol. 153:263-272(2001).
CC -!- FUNCTION: Component of tight junction (TJ) strands.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the claudin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Component of tight junction (TJ) strands.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- DISEASE: Haploinsufficiency of CLDN4 may be the cause of certain cardiovascular and musculo-skeletal abnormalities observed in Williams-Beuren syndrome (WBS), a rare developmental disorder. It is a contiguous gene deletion syndrome involving genes from chromosome band 7q11.23.
CC -!- SIMILARITY: Belongs to the claudin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC
CC EMBL; AB000712; BAA22984.1; -.
DR EMBL; BC000671; AAH00671.1; -.
DR Genew; HGNC:2046; CLDN4.
DR MIM; 602909; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004888; F:transmembrane receptor activity; TAS.
DR GO; GO:0009405; P:pathogenesis; TAS.
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR006188; Claudin reg.
DR InterPro; IPR004031; PMP22 Claudin.
DR Pfam; PF00822; PMP22 Claudin; 1.
DR PRINTS; PR01077; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN; 1.
KW Tight junction; Transmembrane; Williams-Beuren syndrome.
FT TRANSMEM 8 28 POTENTIAL.
FT TRANSMEM 82 102 POTENTIAL.
FT TRANSMEM 118 138 POTENTIAL.
FT TRANSMEM 161 181 POTENTIAL.
FT SEQUENCE 209 AA; 22077 MW; 0659A93AA5F0E4C5 CRC64;
SQ

Query Match 4.0%; Score 9; DB 1; Length 209;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 WEGLWMNCV 55
Db 47 WEGLWMNCV 55
|||||

RESULT 6
CLD4_MOUSE STANDARD; PRT; 210 AA.
ID CLD4_MOUSE STANDARD; PRT; 210 AA.
AC O35054;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Claudin-4 (Clostridium perfringens enterotoxin receptor) (CPE-receptor) (CPE-R).
GN CLDN4 OR CPETR1 OR CPER.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97476271; PubMed=9334247;
RA Katakura J., Sugiyama H., Inoue N., Horiguchi Y., Matsuda M., Sugimoto N.;
RT "Clostridium perfringens enterotoxin utilizes two structurally related membrane proteins as functional receptors in vivo.";
RL J. Biol. Chem. 272:26652-26658(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99110921; PubMed=9892664;
RA Morita K., Furuse M., Fujimoto K., Tsukita S.;


```
DR EMBL; AF358908; AAK51434.1; -.
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR006188; Claudin reg.
DR InterPro; IPR004031; PMP22 Claudin.
DR Pfam; PF00822; PMP22 Claudin; 1.
DR PRINTS; PR01077; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN; 1.
KW Tight junction; Transmembrane.
FT TRANSMEM 9 29 POTENTIAL.
FT TRANSMEM 81 101 POTENTIAL.
FT TRANSMEM 116 136 POTENTIAL.
FT TRANSMEM 160 180 POTENTIAL.
SQ SEQUENCE 218 AA; 23148 MW; 907104E36F50DA70 CRC64;

Query Match 4.0%; Score 9; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 WEGLWMNCV 55
Db 46 WEGLWMNCV 54

RESULT 8
CLD3_MOUSE
ID CLD3_MOUSE STANDARD; PRT; 219 AA.
AC Q9Z0G9; Q91X40;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Claudin-3 (Clostridium perfringens enterotoxin receptor 2) (CPE-
DE receptor 2) (CPE-R 2).
GN CLDN3 OR CPETR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=99097345; PubMed=9878248;
RA Paperna T., Peoples R., Wang Y.K., Kaplan P., Francke U.;
RT "Genes for the CPE receptor (CPETR1) and the human homolog of RVPI
RT (CPETR2) are localized within the Williams-Beuren syndrome deletion.";
RL Genomics 54:453-459(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=99110921; PubMed=9892664;
RA Morita K., Furuse M., Fujimoto K., Tsukita S.;
RT "Claudin multigene family encoding four-transmembrane domain protein
RT components of tight junction strands.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:511-516(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Component of tight junction (TJ) strands.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9Z0G9-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9Z0G9-2; Sequence=VSP_001101;
CC Note=No experimental confirmation available;
CC -!- SIMILARITY: Belongs to the claudin family.

-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; AF095905; AAD14608.1; -.
DR EMBL; AF087821; AAD09756.1; -.
DR EMBL; BC012650; AAH12650.1; -.
DR MGD; MGI:1329044; Cldn3.
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR006188; Claudin reg.
DR InterPro; IPR004031; PMP22 Claudin.
DR Pfam; PF00822; PMP22 Claudin; 1.
DR PRINTS; PR01077; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN; 1.
KW Tight junction; Transmembrane; Alternative splicing.
FT TRANSMEM 9 29 POTENTIAL.
FT TRANSMEM 81 101 POTENTIAL.
FT TRANSMEM 116 136 POTENTIAL.
FT TRANSMEM 160 180 POTENTIAL.
FT VARSPLIC 72 91 Missing (in isoform 2).
FT /FTid=VSP_001101.
SQ SEQUENCE 219 AA; 23284 MW; 62F67810D9B9BD37 CRC64;

Query Match 4.0%; Score 9; DB 1; Length 219;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 WEGLWMNCV 55
Db 46 WEGLWMNCV 54

RESULT 9
CLD3_RAT
ID CLD3_RAT STANDARD; PRT; 219 AA.
AC Q63400;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Claudin-3 (Ventral prostate.1 protein) (RVPI).
GN CLDN3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92130987; PubMed=1723140;
RA Brieht M.M., Miesfeld R.L.;
RT "Isolation and characterization of transcripts induced by androgen
RT withdrawal and apoptotic cell death in the rat ventral prostate.";
RL Mol. Endocrinol. 5:1381-1388(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Keen T.J., Inglehearn C.F.;
RT Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
```

CC -!- FUNCTION: Component of tight junction (TJ) strands.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the claudin family.
CC
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M74067; AAA41760.1; --
CC EMBL; AJ011656; CAA09727.1; --
CC InterPro; IPR006187; Claudin.
CC InterPro; IPR006188; Claudin reg.
CC InterPro; IPR004031; PMP22 Claudin.
CC Pfam; PF00822; PMP22 Claudin; 1.
CC PRINTS; PR01077; CLAUDIN.
CC PROSITE; PS01346; CLAUDIN; 1.
KW Tight junction; Transmembrane.
FT TRANSMEM 9 29 POTENTIAL.
FT TRANSMEM 81 101 POTENTIAL.
FT TRANSMEM 116 136 POTENTIAL.
FT TRANSMEM 162 182 POTENTIAL.
FT CONFLICT 4 4 G -> S (IN REF. 1).
FT CONFLICT 55 55 MISSING (IN REF. 1).
FT CONFLICT 217 219 DYV -> TTSEPGARTPHHHYQPSMYTPRPACSLASETT
FT PPSRRLQTPRSLLARLEDRQGVFPSPVAT (IN REF.
FT 1).
SQ SEQUENCE 219 AA; 23314 MW; 820CC6BFC20D122D CRC64;

Query Match 4.0%; Score 9; DB 1; Length 219;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 WEGLWMNCV 55
| | | | |
Db 46 WEGLWMNCV 54

RESULT 10
CLD3_HUMAN
ID CLD3_HUMAN STANDARD; PRT; 220 AA.
AC O1551;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Claudin-3 (Clostridium perfringens enterotoxin receptor 2) (CPE-
DE receptor 2) (CPE-R 2) (Ventral prostate.1 protein homolog) (HRVP1).
GN CLDN3 OR CPETR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98110580; PubMed=9441748;
RA Peacock R.E., Keen T.J., Inglehearn C.F.;
RT "Analysis of a human gene homologous to rat ventral prostate.1
RT protein.";
RL Genomics 46:443-449(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97476271; PubMed=9334247;
RA Katakura J., Sugiyama H., Inoue N., Horiguchi Y., Matsuda M.,
RA Sugimoto N.;
RT "Clostridium perfringens enterotoxin utilizes two structurally related
RT membrane proteins as functional receptors in vivo.";
RL J. Biol. Chem. 272:26552-26658(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;

RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Component of tight junction (TJ) strands.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- DISEASE: Haploinsufficiency of CLDN3 may be the cause of certain
CC cardiovascular and musculo-skeletal abnormalities observed in
CC Williams-Beuren syndrome (WBS), a rare developmental disorder. It
CC is a contiguous gene deletion syndrome involving genes from
CC chromosome band 7q11.23.
CC
CC -!- SIMILARITY: Belongs to the claudin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF007189; AAC78277.1; --
CC EMBL; AB000714; BAA22986.1; --
CC EMBL; BC016056; AAH16056.1; --
CC Genew; HGNC:2045; CLDN3.
CC MIM; 602910; --
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0004988; F:transmembrane receptor activity; TAS.
CC InterPro; IPR006187; Claudin.
CC InterPro; IPR006188; Claudin reg.
CC InterPro; IPR004031; PMP22 Claudin.
CC Pfam; PF00822; PMP22 Claudin; 1.
CC PRINTS; PR01077; CLAUDIN.
CC PROSITE; PS01346; CLAUDIN; 1.
KW Tight junction; Transmembrane; Williams-Beuren syndrome.
FT TRANSMEM 9 29 POTENTIAL.
FT TRANSMEM 81 101 POTENTIAL.
FT TRANSMEM 116 136 POTENTIAL.
FT TRANSMEM 160 180 POTENTIAL.
SQ SEQUENCE 220 AA; 23318 MW; 1C826EFFF1563C56 CRC64;

Query Match 4.0%; Score 9; DB 1; Length 220;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 WEGLWMNCV 55
| | | | |
Db 46 WEGLWMNCV 54

RESULT 11
CLDH_HUMAN
ID CLDH_HUMAN STANDARD; PRT; 224 AA.
AC P56750;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)

```
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Claudin-17.
GN CLDN17.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Keen T.J., Inglehearn C.F.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20289799; PubMed=10830953;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
RA Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
RA Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Sasaki T., Nagamine K., Mitsuyma S., Antonarakis S.E.,
RA Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
RA Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA Lehrach H., Reinhardt R., Yaspo M.-L.;
RT "The DNA sequence of human chromosome 21.";
RL Nature 405:311-319(2000).
CC -!- FUNCTION: Component of tight junction (TJ) strands.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the claudin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ250712; CAB60616.1; -.
DR EMBL; AP001707; BAA95566.1; -.
DR Genew; HGNC:2038; CLDN17.
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR006188; Claudin reg.
DR InterPro; IPR004031; PMP22_Claudin.
DR Pfam; PF00822; PMP22_Claudin; 1.
DR PRINTS; PR01077; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN; 1.
KW Tight junction; Transmembrane.
FT TRANSMEM 8 28
FT TRANSMEM 82 102
FT TRANSMEM 125 145
FT TRANSMEM 165 185
SQ SEQUENCE 224 AA; 24603 MW; 1833ED3178B7F63A CRC64;
Query Match 3.6%; Score 8; DB 1; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 28 PQWRVSFAF 35
Db 28 PQWRVSFAF 35
|||||
RESULT 12
ID G17M_BACSU STANDARD; PRT; 115 AA.
AC P80241;
DT 01-FEB-1995 (Rel. 31, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE General stress protein 17M (GSP17M).
```

```
GN YFLT OR BSU07550.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AC327;
RX MEDLINE=97417488; PubMed=9272861;
RA Yamamoto H., Uchiyama S., Nugroho F.A., Sekiguchi J.;
RT "Cloning and sequencing of a 35.7 kb in the 70 degree-73 degree region
RT of the Bacillus subtilis genome reveal genes for a new two-component
RT system, three spore germination proteins, an iron uptake system and a
RT general stress response protein.";
RL Gene 194:191-199(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=168;
RC MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardiniois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
RN [3]
RP SEQUENCE OF 1-21.
RC STRAIN=168 / IS58;
RX MEDLINE=94282319; PubMed=8012595;
RA Voelker U., Engelmann S., Maul B., Riethdorf S., Voelker A.,
RA Schmid R., Mach H., Hecker M.;
RT "Analysis of the induction of general stress proteins of Bacillus
RT subtilis.";
RL Microbiology 140:741-752(1994).
CC -!- INDUCTION: By heat shock, salt stress, oxidative stress, glucose
CC limitation and oxygen limitation.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D86417; BAA22314.1; -.
DR EMBL; Z99108; CAB12584.1; -.
DR PIR; G69811; G69811.
DR Subtilist; BG19020; yflt.
```


DR PRINTS; PR01077; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN; 1.
KW Tight Junction; Transmembrane.
FT TRANSMEM 8 28 POTENTIAL.
FT TRANSMEM 81 101 POTENTIAL.
FT TRANSMEM 114 134 POTENTIAL.
FT TRANSMEM 159 179 POTENTIAL.
SQ SEQUENCE 209 AA; 22091 MW; C413143811853D58 CRC64;

Query Match 3.1%; Score 7; DB 1; Length 209;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 144 IIRDFYN 150
Db 142 IIRDFYN 148

Search completed: September 1, 2004, 16:58:39
Job time : 14 secs

U.S. 171

Blank Check

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2004, 16:54:59 ; Search time 55 Seconds
(without alignments)
1155.876 Million cell updates/sec

Title: US-10-063-732-120
Perfect score: 225
Sequence: 1 MATHALEITAGLFLGGVMVG.....QKSYHTGKKSFSVYSRSQYV 225

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 6

Total number of hits satisfying chosen parameters: 4883

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	225	100.0	225	3	AA99433	Aay99433 Human PRO
2	225	100.0	225	4	AAB66182	Aab66182 Protein o
3	225	100.0	225	4	AAM78572	Aam78572 Human PRO
4	225	100.0	225	4	AAU29202	Aau29202 Human PRO
5	225	100.0	225	4	AAB87585	Aab87585 Human PRO
6	225	100.0	225	4	AAG89285	Aag89285 Human sec
7	225	100.0	225	5	ABG95910	Abg95910 Human sec
8	225	100.0	225	6	ABU58578	Abu58578 Human PRO
9	225	100.0	225	6	ABU88126	Abu88126 Novel hum
10	225	100.0	225	6	ABU84441	Abu84441 Human sec
11	225	100.0	225	6	ABR66315	ABr66315 Human sec
12	225	100.0	225	6	ABR65705	ABr65705 Human sec
13	225	100.0	225	6	ABU99645	ABu99645 Human sec
14	225	100.0	225	6	ABU82884	ABu82884 Human PRO
15	225	100.0	225	6	ABU90005	ABu90005 Novel hum
16	225	100.0	225	6	ABR68254	ABr68254 Human sec
17	225	100.0	225	6	ABU96307	ABu96307 Novel hum
18	225	100.0	225	6	ABU92738	ABu92738 Human sec
19	225	100.0	225	6	ABO08815	ABo08815 Human sec
20	225	100.0	225	6	ABO02867	ABo02867 Human sec
21	225	100.0	225	6	ABR75021	ABr75021 Human sec
22	225	100.0	225	6	ABR94783	ABr94783 Human sec
23	225	100.0	225	6	ABU85756	ABu85756 Human PRO
24	225	100.0	225	6	ABU98916	ABu98916 Novel hum
25	225	100.0	225	6	ABU98131	ABu98131 Novel hum

26	225	100.0	225	6	ABU91837	Abu91837 Novel hum
27	225	100.0	225	6	ABU89530	Abu89530 Human PRO
28	225	100.0	225	6	ABU86371	Abu86371 Human sec
29	225	100.0	225	6	ABU67584	Abu67584 Human sec
30	225	100.0	225	6	ABU80612	Abu80612 Human PRO
31	225	100.0	225	6	ABU90935	Abu90935 Novel hum
32	225	100.0	225	6	ABO33994	ABo33994 Human sec
33	225	100.0	225	6	ABR99530	ABr99530 Human sec
34	225	100.0	225	6	ABR98920	ABr98920 Human sec
35	225	100.0	225	6	ABO16443	ABo16443 Human sec
36	225	100.0	225	6	ABR92343	ABr92343 Human sec
37	225	100.0	225	6	ABO18984	ABo18984 Human sec
38	225	100.0	225	6	ABR78405	ABr78405 Human sec
39	225	100.0	225	6	ABU72011	ABu72011 Novel hum
40	225	100.0	225	6	ABU85141	ABu85141 Novel hum
41	225	100.0	225	6	ABO00280	ABo00280 Novel hum
42	225	100.0	225	6	ABO11612	ABo11612 Human sec
43	225	100.0	225	6	ABO02257	ABo02257 Human sec
44	225	100.0	225	6	ABU88831	ABu88831 Novel hum
45	225	100.0	225	6	ABU83526	ABu83526 Human sec

ALIGNMENTS

RESULT 1
AA99433
ID AA99433 standard; protein; 225 AA.
XX
AC AA99433;
XX
DT 08-AUG-2000 (first entry)
XX
DE Human PRO1573 (UNQ779) amino acid sequence SEQ ID NO:328.
XX
KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis; transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
XX
OS Homo sapiens.
XX
PN WO200012708-A2.
XX
PD 09-MAR-2000.
XX
PF 01-SEP-1999; 99WO-US020111.
XX
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099536P.
PR 09-SEP-1998; 98US-0099596P.
PR 09-SEP-1998; 98US-0099602P.
PR 09-SEP-1998; 98US-0099642P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099808P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 10-SEP-1998; 98US-0099816P.
PR 15-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100661P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.

AC AAB66182;
XX
DT 02-APR-2001 (first entry)
XX
DE Protein of the invention #94.
XX
KW Secreted; transmembrane; gene therapy.
XX
OS Unidentified.
XX
PN WO200078961-A1.
XX
PD 28-DEC-2000.
XX
PF 18-FEB-2000; 2000WO-US004342.
XX
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX
DR WPI; 2001-071395/08.
XX
XX Secreted and transmembrane proteins and nucleic acids designated PRO,
PT useful as hybridization probes, in chromosome and gene mapping and gene
PT therapy.
XX
PS Claim 1; Fig 188; 787pp; English.
XX
CC The present invention relates to secreted and transmembrane proteins.
CC These proteins and the DNA encoding them may be used as hybridization
CC probes, in chromosome and gene mapping and in the generation of anti-
CC sense RNA and DNA. They may also be used to generate either
CC transgenic animals or knockout animals which are in turn useful for
CC development and screening of therapeutically useful reagents. The nucleic
CC acids may also be used in gene therapy
XX
SQ Sequence 225 AA;

Query Match 100.0%; Score 225; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 3.2e-212;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNVFENFWEGLWMNCVRQANI 60
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNVFENFWEGLWMNCVRQANI 60

Qy 61 RMQCKIYDLSLLALSPDLQAARGLMCAASVMSFLAFMMAILGKCTRCTGDNEKVAHILL 120
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 RMQCKIYDLSLLALSPDLQAARGLMCAASVMSFLAFMMAILGKCTRCTGDNEKVAHILL 120

Qy 121 TAGIIFIITGMVLIPIVSWVANAIIRDYFNSIVNVAQKRELGEALYLGWTTALVLIVGGA 180
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 TAGIIFIITGMVLIPIVSWVANAIIRDYFNSIVNVAQKRELGEALYLGWTTALVLIVGGA 180

Qy 181 LFCCVFCCKEKKSSRYSIPISTRTTQKSYHTGKKSPSVYSRSQYV 225
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 LFCCVFCCKEKKSSRYSIPISTRTTQKSYHTGKKSPSVYSRSQYV 225

RESULT 3
AAM78572
ID AAM78572 standard; protein; 225 AA.
XX
AC AAM78572;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 1234.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US004098.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00598075.
PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI; 2001-476283/51.
DR N-PSDB; AAK51705.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
XX
PS Claim 20; Page 3493-3494; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
SQ Sequence 225 AA;

Query Match 100.0%; Score 225; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 3.2e-212;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNVFENFWEGLWMNCVRQANI 60
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNVFENFWEGLWMNCVRQANI 60

Qy 61 RMQCKIYDLSLLALSPDLQAARGLMCAASVMSFLAFMMAILGKCTRCTGDNEKVAHILL 120
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 RMQCKIYDLSLLALSPDLQAARGLMCAASVMSFLAFMMAILGKCTRCTGDNEKVAHILL 120

QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDYFNSIVNVAQKRELGEALYLGTALVLIIVGGA 180
Db 121 TAGIIFIITGMVVLIPVSWVANAIIRDYFNSIVNVAQKRELGEALYLGTALVLIIVGGA 180
QY 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYRSQYV 225
Db 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYRSQYV 225

RESULT 4
AAU29202
ID AAU29202 standard; protein; 225 AA.
XX
AC AAU29202;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human PRO polypeptide sequence #179.
XX
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
OS Homo sapiens.
XX
FN WO200168848-A2.
XX
PD 20-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006520.
XX
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 06-MAR-2000; 2000US-0186968P.
PR 14-MAR-2000; 2000US-0189320P.
PR 14-MAR-2000; 2000US-0189328P.
PR 15-MAR-2000; 2000WO-US006884.
PR 21-MAR-2000; 2000US-0190828P.
PR 21-MAR-2000; 2000US-0191007P.
PR 21-MAR-2000; 2000US-0191048P.
PR 21-MAR-2000; 2000US-0191314P.
PR 28-MAR-2000; 2000US-0192655P.
PR 29-MAR-2000; 2000US-0193032P.
PR 29-MAR-2000; 2000US-0193053P.
PR 30-MAR-2000; 2000WO-US008439.
PR 04-APR-2000; 2000US-0194449P.
PR 04-APR-2000; 2000US-0194647P.
PR 11-APR-2000; 2000US-0195975P.
PR 11-APR-2000; 2000US-0196000P.
PR 11-APR-2000; 2000US-0196187P.
PR 11-APR-2000; 2000US-0196690P.
PR 11-APR-2000; 2000US-0196820P.
PR 18-APR-2000; 2000US-0198121P.
PR 18-APR-2000; 2000US-0198585P.
PR 25-APR-2000; 2000US-0199397P.
PR 25-APR-2000; 2000US-0199550P.
PR 25-APR-2000; 2000US-0199654P.
PR 03-MAY-2000; 2000US-0201516P.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
XX

PA (GETH) GENENTECH INC.
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2001-602746/68.
DR N-PSDB; AAS46103.
XX
PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumors, such as prostate and breast tumors, in mammals and to
PT screen for modulators of the compounds.
XX
PS Claim 11; Fig 358; 774pp; English.
XX
CC Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC The PRO polypeptides and their associated nucleic acids can be used to
CC detect the presence of a tumour in a mammal by comparing the level of
CC expression of a PRO polypeptide in a test sample of cells from the animal
CC and a control sample of normal cells, whereby a higher level of
CC expression in the test sample indicates the presence of a tumour in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders
XX
SQ Sequence 225 AA;
Query Match 100.0%; Score 225; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 3.2e-212;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATHALEIAGLFLGGVGMVGTAVTMPQWRVSFAFIENNIVVFENFWEGLMNCVRQANI 60
Db 1 MATHALEIAGLFLGGVGMVGTAVTMPQWRVSFAFIENNIVVFENFWEGLMNCVRQANI 60
QY 61 RMOCKIYDSLALSPDLQAARGLMCAASVMSFLAFMAILGKCTRCTGDNEKVKAHILL 120
Db 61 RMOCKIYDSLALSPDLQAARGLMCAASVMSFLAFMAILGKCTRCTGDNEKVKAHILL 120
QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDYFNSIVNVAQKRELGEALYLGTALVLIIVGGA 180
Db 121 TAGIIFIITGMVVLIPVSWVANAIIRDYFNSIVNVAQKRELGEALYLGTALVLIIVGGA 180
QY 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYRSQYV 225
Db 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYRSQYV 225
RESULT 5
AAB87585
ID AAB87585 standard; protein; 225 AA.
XX
AC AAB87585;
XX
DT 15-MAY-2001 (first entry)
XX
DE Human PRO1573.
XX
KW Human; PRO protein; mapping.
XX
OS Homo sapiens.
XX
PN WO200116318-A2.
XX
PD 08-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-US023328.

XX 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 07-DEC-1999; 99US-0169495P.
PR 09-DEC-1999; 99US-0170262P.
PR 11-JAN-2000; 2000US-0175481P.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 03-MAR-2000; 2000US-0187202P.
PR 21-MAR-2000; 2000US-0191007P.
PR 30-MAR-2000; 2000WO-US008439.
PR 25-APR-2000; 2000US-0199397P.
PR 22-MAY-2000; 2000WO-US014042.
PR 05-JUN-2000; 2000US-0209832P.
XX (GETH) GENENTECH INC.
PA
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2001-183260/18.
DR N-PSDB; AAF92117.
XX
PT Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
PT biology, including use as hybridization probes, and in chromosome and
PT gene mapping.
XX
PS Claim 12; Fig 120; 278pp; English.
XX
CC The present sequence is a human PRO polypeptide (secreted and
CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
CC anti-PRO antibodies are useful for preparation of a medicament useful in
CC the treatment of a condition which is responsive to the PRO protein,
CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
CC employed as molecular weight markers for protein electrophoresis. The PRO
CC coding sequence has applications in molecular biology, including use as
CC hybridisation probes, and in chromosome and gene mapping
XX
SQ Sequence 225 AA;

Query Match 100.0%; Score 225; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 3.2e-212;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNIIVFENFWEGLMNCVRQANI 60
Db |||||||
QY 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNIIVFENFWEGLMNCVRQANI 60
Db |||||||
QY 61 RMOCKIYDSSLALSPDLQAARGLMCAASVMSFLAFMAILGKCTRCTGDNEKVKAHILL 120
Db |||||||
QY 61 RMOCKIYDSSLALSPDLQAARGLMCAASVMSFLAFMAILGKCTRCTGDNEKVKAHILL 120
QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGTWTTALVLIIVGGA 180
Db |||||||
QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGTWTTALVLIIVGGA 180
QY 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQYV 225
Db |||||||
181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQYV 225

RESULT 6
AAG89285
ID AAG89285 standard; protein; 225 AA.
XX
AC AAG89285;
XX
DT 11-SEP-2001 (first entry)
XX
DE Human secreted protein, SEQ ID NO: 405.
XX

KW Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;
KW GENSET.
XX
OS Homo sapiens.
XX
PN WO200142451-A2.
XX
PD 14-JUN-2001.
XX
PF 07-DEC-2000; 2000WO-IB001938.
XX
PR 08-DEC-1999; 99US-0169629P.
PR 06-MAR-2000; 2000US-0187470P.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Bougueleret L, Jobert S;
XX
DR WPI; 2001-367870/38.
DR N-PSDB; AAH64888.
XX
PT Full length GENSET human nucleic acids encoding potentially secreted
PT proteins, useful in gene therapy and vaccination against a variety of
PT diseases, and for diagnosis of those diseases.
XX
PS Claim 21; Page 885-886; 921pp; English.
XX
CC The invention relates to full length GENSET human nucleic acids encoding
CC potentially secreted proteins. The nucleic acids and the polypeptides
CC they encode may be used in the prevention, treatment and diagnosis of
CC diseases associated with inappropriate GENSET gene expression. For
CC example, they be used to treat disorders associated with decreased GENSET
CC gene expression by rectifying mutations or deletions in a patient's
CC genome that affect the activity of GENSET or by supplementing the
CC patients own production of GENSET polypeptides. Conversely, antisense
CC nucleic acid molecules may be administered to down regulate GENSET
CC expression by binding with the cells' own genes and preventing their
CC expression. The sense and antisense nucleic acids may also be used as DNA
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar nucleic acid sequences in samples, and hence to determine which
CC patients may be in need of restorative therapy. The GENSET polypeptides
CC may be used as antigens in the production of antibodies and in assays to
CC identify modulators (agonists and antagonists) of GENSET polypeptide
CC expression and activity. The present sequence is a GENSET polypeptide of
CC the invention
XX
SQ Sequence 225 AA;

Query Match 100.0%; Score 225; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 3.2e-212;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNIIVFENFWEGLMNCVRQANI 60
Db |||||||
QY 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNIIVFENFWEGLMNCVRQANI 60
Db |||||||
QY 61 RMOCKIYDSSLALSPDLQAARGLMCAASVMSFLAFMAILGKCTRCTGDNEKVKAHILL 120
Db |||||||
QY 61 RMOCKIYDSSLALSPDLQAARGLMCAASVMSFLAFMAILGKCTRCTGDNEKVKAHILL 120
QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGTWTTALVLIIVGGA 180
Db |||||||
QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGTWTTALVLIIVGGA 180
QY 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQYV 225
Db |||||||
181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQYV 225

RESULT 7
ABG95910
ID ABG95910 standard; protein; 225 AA.
XX

AC ABG95910;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human secreted/transmembrane protein PRO1573.
XX
KW Human; secreted protein; transmembrane protein; antirheumatic;
KW antiarthritic; osteopathic; sports-related joint problem;
KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.
XX
OS Homo sapiens.
XX
PN US2002119130-A1.
XX
PD 29-AUG-2002.
XX
PF 06-DEC-2001; 2001US-00006867.
XX
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0064215P.
PR 22-APR-1998; 98US-0082797P.
PR 29-APR-1998; 98US-0083495P.
PR 15-MAY-1998; 98US-0085579P.
PR 02-JUN-1998; 98US-0087759P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 11-JUN-1998; 98US-0088863P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089653P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 24-JUN-1998; 98US-0090444P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 02-JUL-1998; 98US-0091628P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097971P.
PR 01-SEP-1998; 98US-0098749P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100930P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101475P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101916P.
PR 30-SEP-1998; 98US-0102570P.
PR 06-OCT-1998; 98US-0103449P.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.

PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021194.
PR 22-DEC-1999; 99WO-US030720.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005501.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032378.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.

(GETH) GENENTECH INC.

Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

WPI; 2002-731348/79.
N-PSDB; ABS74437.

New isolated secreted and transmembrane PRO polypeptide useful for modulating biological activity of a cell, or for treating sports-related joint problems, osteoarthritis or rheumatoid arthritis.

Claim 20; Fig 120; 399pp; English.

The invention relates to an isolated secreted and transmembrane PRO polypeptide having 80 % sequence identity to a sequence appearing as ABG95851-ABG95934 or their associated signal peptide, or a sequence of an extracellular domain of the proteins with their associated signal peptide or lacking its associated signal peptide. Also included are the nucleic acids encoding the proteins, vectors, host cells, fusion proteins and antibodies which specifically bind to the proteins. The proteins are useful for detecting a polypeptide designated as A, B, C or D in a sample suspected of containing an A, B, C or D polypeptide, by contacting the sample with a polypeptide designated as E, F, G, H or I (or vice versa) and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide conjugate in the sample, where the formation of the conjugate is indicative of the presence of an A, B, C or D polypeptide in the sample, where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801 polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G, H or I polypeptide is labeled with a detectable label or is attached to a solid support. The proteins are useful for linking a bioactive molecule to a cell expressing a polypeptide designated as A, B, C or D or E, F, G, H or I. The bioactive molecule is a toxin, a radiolabel or an antibody. The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H, or I, or antibodies against them are useful for modulating a biological activity of a cell expressing a polypeptide designated as A, B, C or D or E, F, G, H, or I. The cell is killed. The proteins are useful for identifying agonists or antagonists, for the preparation of a medicament useful in the treatment of a condition which is responsive to the proteins, as molecular weight markers for protein electrophoresis purposes, and as therapeutic agents for treating sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis. Nucleic acids encoding the proteins are useful as hybridisation probes, in chromosome and gene mapping, in the generation of anti-sense RNA and DNA, for the preparation of the proteins, to generate transgenic or knockout animals which are useful in the development and screening of therapeutic useful reagents, for chromosome

CC identification, and in gene therapy. The antibody is useful as a
CC therapeutic agent, in a diagnostic assay and for affinity purification of
CC the protein from recombinant cell culture natural sources. The present
CC sequence represents a novel secreted or transmembrane protein of the
CC invention
XX
SQ Sequence 225 AA;

Query Match 100.0%; Score 225; DB 5; Length 225;
Best Local Similarity 100.0%; Pred. No. 3.2e-212;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATHALEIAGLFLGGVGMGTVAVTVMQWRVSAFIENNVFENFWEGLMNCVRQANI 60
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 MATHALEIAGLFLGGVGMGTVAVTVMQWRVSAFIENNVFENFWEGLMNCVRQANI 60
QY 61 RMQCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 RMQCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120
QY 121 TAGIIFIITGMVVLIPVSWANAIIRDYFNSIVNVAQKRELGEALYLGWTTALVLIVGGA 180
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 TAGIIFIITGMVVLIPVSWANAIIRDYFNSIVNVAQKRELGEALYLGWTTALVLIVGGA 180
QY 181 LFCCVFCNEKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQYV 225
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 LFCCVFCNEKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQYV 225

RESULT 8
ABU58578
ID ABU58578 standard; protein; 225 AA.
XX
AC ABU58578;
XX
DT 15-APR-2003 (first entry)
XX
DE Human PRO polypeptide #179.
XX
KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrg therapy.
XX
OS Homo sapiens.
XX
PN US2003027272-A1.
XX
PD 06-FEB-2003.
XX
PF 21-JUN-2002; 2002US-00176492.
XX

PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066772P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.

PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078939P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080333P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081838P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083559P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085700P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087208P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 24-JUN-1998; 98US-0090429P.

PR	24-JUN-1998;	98US-0090435P.
PR	24-JUN-1998;	98US-0090444P.
PR	24-JUN-1998;	98US-0090461P.
PR	24-JUN-1998;	98US-0090535P.
PR	24-JUN-1998;	98US-0090540P.
PR	25-JUN-1998;	98US-0090676P.
PR	25-JUN-1998;	98US-0090688P.
PR	25-JUN-1998;	98US-0090690P.
PR	25-JUN-1998;	98US-0090694P.
PR	25-JUN-1998;	98US-0090695P.
PR	25-JUN-1998;	98US-0090696P.
PR	26-JUN-1998;	98US-00105413.
PR	26-JUN-1998;	98US-0090862P.
PR	26-JUN-1998;	98US-0090863P.
PR	26-JUN-1998;	98US-0091010P.
PR	01-JUL-1998;	98US-0091359P.
PR	01-JUL-1998;	98US-0091544P.
PR	02-JUL-1998;	98US-0091478P.
PR	02-JUL-1998;	98US-0091486P.
PR	02-JUL-1998;	98US-0091626P.
PR	02-JUL-1998;	98US-0091628P.
PR	02-JUL-1998;	98US-0091632P.
PR	24-JUL-1998;	98US-0094006P.
PR	04-AUG-1998;	98US-0095282P.
PR	10-AUG-1998;	98US-0095998P.
PR	10-AUG-1998;	98US-0096012P.
PR	17-AUG-1998;	98US-0096757P.
PR	17-AUG-1998;	98US-0096766P.
PR	17-AUG-1998;	98US-0096867P.
PR	17-AUG-1998;	98US-0096891P.
PR	17-AUG-1998;	98US-0096897P.
PR	18-AUG-1998;	98US-0096949P.
PR	18-AUG-1998;	98US-0096959P.
PR	18-AUG-1998;	98US-0097022P.
PR	26-AUG-1998;	98US-0097952P.
PR	26-AUG-1998;	98US-0097954P.
PR	26-AUG-1998;	98US-0097955P.
PR	26-AUG-1998;	98US-0097971P.
PR	26-AUG-1998;	98US-0097974P.
PR	01-SEP-1998;	98US-0098014P.
PR	01-SEP-1998;	98US-0098716P.
PR	01-SEP-1998;	98US-0098723P.
PR	02-SEP-1998;	98US-0098803P.
PR	02-SEP-1998;	98US-0098821P.
PR	02-SEP-1998;	98US-0098843P.
PR	09-SEP-1998;	98US-0099602P.
PR	10-SEP-1998;	98US-0099741P.
PR	10-SEP-1998;	98US-0099754P.
PR	10-SEP-1998;	98US-0099763P.
PR	10-SEP-1998;	98US-0099812P.
PR	15-SEP-1998;	98US-0100388P.
PR	16-SEP-1998;	98US-0100662P.
PR	16-SEP-1998;	98US-0100664P.
PR	16-SEP-1998;	98US-0101751P.
PR	16-SEP-1998;	98WO-US019330.
PR	17-SEP-1998;	98US-0100683P.
PR	17-SEP-1998;	98US-0100684P.
PR	17-SEP-1998;	98US-0100919P.
PR	17-SEP-1998;	98US-0100930P.
PR	18-SEP-1998;	98US-0100849P.
PR	18-SEP-1998;	98US-0101014P.
PR	18-SEP-1998;	98US-0101068P.
PR	23-SEP-1998;	98US-0101471P.
PR	23-SEP-1998;	98US-0101472P.
PR	23-SEP-1998;	98US-0101475P.
PR	23-SEP-1998;	98US-0101477P.
PR	24-SEP-1998;	98US-0101738P.
PR	24-SEP-1998;	98US-0101739P.
PR	24-SEP-1998;	98US-0101743P.
PR	24-SEP-1998;	98US-0101922P.
PR	25-SEP-1998;	98US-0101786P.
PR	29-SEP-1998;	98US-0102207P.
PR	24-JUN-1998;	98US-0090435P.
PR	24-JUN-1998;	98US-0090444P.
PR	24-JUN-1998;	98US-0090461P.
PR	24-JUN-1998;	98US-0090535P.
PR	24-JUN-1998;	98US-0090540P.
PR	25-JUN-1998;	98US-0090676P.
PR	25-JUN-1998;	98US-0090688P.
PR	25-JUN-1998;	98US-0090690P.
PR	25-JUN-1998;	98US-0090694P.
PR	25-JUN-1998;	98US-0090695P.
PR	25-JUN-1998;	98US-0090696P.
PR	26-JUN-1998;	98US-00105413.
PR	26-JUN-1998;	98US-0090862P.
PR	26-JUN-1998;	98US-0090863P.
PR	26-JUN-1998;	98US-0091010P.
PR	01-JUL-1998;	98US-0091359P.
PR	01-JUL-1998;	98US-0091544P.
PR	02-JUL-1998;	98US-0091478P.
PR	02-JUL-1998;	98US-0091486P.
PR	02-JUL-1998;	98US-0091626P.
PR	02-JUL-1998;	98US-0091628P.
PR	02-JUL-1998;	98US-0091632P.
PR	24-JUL-1998;	98US-0094006P.
PR	04-AUG-1998;	98US-0095282P.
PR	10-AUG-1998;	98US-0095998P.
PR	10-AUG-1998;	98US-0096012P.
PR	17-AUG-1998;	98US-0096757P.
PR	17-AUG-1998;	98US-0096766P.
PR	17-AUG-1998;	98US-0096867P.
PR	17-AUG-1998;	98US-0096891P.
PR	17-AUG-1998;	98US-0096897P.
PR	18-AUG-1998;	98US-0096949P.
PR	18-AUG-1998;	98US-0096959P.
PR	18-AUG-1998;	98US-0097022P.
PR	26-AUG-1998;	98US-0097952P.
PR	26-AUG-1998;	98US-0097954P.
PR	26-AUG-1998;	98US-0097955P.
PR	26-AUG-1998;	98US-0097971P.
PR	26-AUG-1998;	98US-0097974P.
PR	01-SEP-1998;	98US-0098014P.
PR	01-SEP-1998;	98US-0098716P.
PR	01-SEP-1998;	98US-0098723P.
PR	02-SEP-1998;	98US-0098803P.
PR	02-SEP-1998;	98US-0098821P.
PR	02-SEP-1998;	98US-0098843P.
PR	09-SEP-1998;	98US-0099602P.
PR	10-SEP-1998;	98US-0099741P.
PR	10-SEP-1998;	98US-0099754P.
PR	10-SEP-1998;	98US-0099763P.
PR	10-SEP-1998;	98US-0099812P.
PR	15-SEP-1998;	98US-0100388P.
PR	16-SEP-1998;	98US-0100662P.
PR	16-SEP-1998;	98US-0100664P.
PR	16-SEP-1998;	98US-0101751P.
PR	16-SEP-1998;	98WO-US019330.
PR	17-SEP-1998;	98US-0100683P.
PR	17-SEP-1998;	98US-0100684P.
PR	17-SEP-1998;	98US-0100919P.
PR	17-SEP-1998;	98US-0100930P.
PR	18-SEP-1998;	98US-0100849P.
PR	18-SEP-1998;	98US-0101014P.
PR	18-SEP-1998;	98US-0101068P.
PR	23-SEP-1998;	98US-0101471P.
PR	23-SEP-1998;	98US-0101472P.
PR	23-SEP-1998;	98US-0101475P.
PR	23-SEP-1998;	98US-0101477P.
PR	24-SEP-1998;	98US-0101738P.
PR	24-SEP-1998;	98US-0101739P.
PR	24-SEP-1998;	98US-0101743P.
PR	24-SEP-1998;	98US-0101922P.
PR	25-SEP-1998;	98US-0101786P.
PR	29-SEP-1998;	98US-0102207P.
PR	29-SEP-1998;	98US-0102240P.
PR	29-SEP-1998;	98US-0102330P.
PR	29-SEP-1998;	98US-0102331P.
PR	30-SEP-1998;	98US-0102487P.
PR	30-SEP-1998;	98US-0102570P.
PR	30-SEP-1998;	98US-0102571P.
PR	01-OCT-1998;	98US-0102684P.
PR	01-OCT-1998;	98US-0102687P.
PR	02-OCT-1998;	98US-0102965P.
PR	06-OCT-1998;	98US-0103258P.
PR	06-OCT-1998;	98US-0103449P.
PR	07-OCT-1998;	98US-00168978.
Query Match 100.0%; Score 225; DB 6; Length 225;		
Best Local Similarity 100.0%; Pred. No. 3.2e-212;		
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	MATHALEIAGLFLGGVGMVGTVAVTVMPOWRVSAFIENNIIVVFENFWEGLMNCVRQANI 60
Db	1	MATHALEIAGLFLGGVGMVGTVAVTVMPOWRVSAFIENNIIVVFENFWEGLMNCVRQANI 60
QY	61	RMOCKIYDSSLALSPDLQAARGLMCAASVMSFLAFMAILGMKCTRCTGDNEKVKAHILL 120
Db	61	RMOCKIYDSSLALSPDLQAARGLMCAASVMSFLAFMAILGMKCTRCTGDNEKVKAHILL 120
QY	121	TAGIIFIITGMVVLIPVSVNANAIIIRDFYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
Db	121	TAGIIFIITGMVVLIPVSVNANAIIIRDFYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
QY	181	LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYRSQYV 225
Db	181	LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYRSQYV 225
RESULT 9		
ABU88126		
ID	ABU88126	standard; protein; 225 AA.
XX	ABU88126;	
XX	07-JUL-2003	(first entry)
DE	Novel human secreted and transmembrane protein PRO1573.	
XX	Human; secreted and transmembrane protein: PRO; gene therapy;	
KW	tumour necrosis factor-alpha release; TNF-alpha release;	
KW	chondrocyte proliferation; chondrocyte differentiation; tumour;	
KW	adrenal tumour; lung tumour; colon tumour; breast tumour;	
KW	prostate tumour; rectal tumour; cervical tumour; liver tumour.	
XX	Homo sapiens.	
OS	US2003032127-A1.	
PN	13-FEB-2003.	
XX	26-JUN-2002; 2002US-00183012.	
PD	18-SEP-1997; 97US-0059263P.	
XX	18-SEP-1997; 97US-0059266P.	
PF	17-OCT-1997; 97US-0062250P.	
XX	21-OCT-1997; 97US-0063486P.	
XX	24-OCT-1997; 97US-0063120P.	
XX	24-OCT-1997; 97US-0063121P.	
XX	28-OCT-1997; 97US-0063540P.	
XX	28-OCT-1997; 97US-0063541P.	
XX	28-OCT-1997; 97US-0063544P.	
XX	28-OCT-1997; 97US-0063564P.	
XX	29-OCT-1997; 97US-0063734P.	
XX	31-OCT-1997; 97US-0063870P.	
XX	31-OCT-1997; 97US-0064103P.	
XX	13-NOV-1997; 97US-0065311P.	
XX	21-NOV-1997; 97US-0066120P.	

PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066772P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078939P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080333P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081838P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083559P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085700P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087208P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.

PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090540P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091632P.
PR 24-JUL-1998; 98US-0094006P.
PR 04-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-0095998P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0097022P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0098014P.
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099602P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099812P.
PR 15-SEP-1998; 98US-0100388P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101475P.

PR	23-SEP-1998;	98US-0101477P.
PR	24-SEP-1998;	98US-0101738P.
PR	24-SEP-1998;	98US-0101739P.
PR	24-SEP-1998;	98US-0101743P.
PR	24-SEP-1998;	98US-0101922P.
PR	25-SEP-1998;	98US-0101786P.
PR	29-SEP-1998;	98US-0102207P.
PR	29-SEP-1998;	98US-0102240P.
PR	29-SEP-1998;	98US-0102330P.
PR	29-SEP-1998;	98US-0102331P.
PR	30-SEP-1998;	98US-0102487P.
PR	30-SEP-1998;	98US-0102570P.
PR	30-SEP-1998;	98US-0102571P.
PR	01-OCT-1998;	98US-0102684P.
PR	01-OCT-1998;	98US-0102687P.
PR	02-OCT-1998;	98US-0102965P.
PR	06-OCT-1998;	98US-0103258P.
Query Match 100.0%; Score 225; DB 6; Length 225;		
Best Local Similarity 100.0%; Pred. No. 3.2e-212;		
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	MATHALEIAGLFLGGVGMGTVAVTMPQWRVSAFIENNIIVVFENFWEGLWMNCVRQANI 60
Db	1	MATHALEIAGLFLGGVGMGTVAVTMPQWRVSAFIENNIIVVFENFWEGLWMNCVRQANI 60
QY	61	RMQCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120
Db	61	RMQCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120
QY	121	TAGIIFIITGMVVLIPVSWANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGA 180
Db	121	TAGIIFIITGMVVLIPVSWANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGA 180
QY	181	LFCCVFCCKNEKSSSYRYSIPSHRITTOKSYHTGKKSPSVYRSQYV 225
Db	181	LFCCVFCCKNEKSSSYRYSIPSHRITTOKSYHTGKKSPSVYRSQYV 225
RESULT 10		
ABU84441		
ID	ABU84441 standard; protein; 225 AA.	
XX	AC ABU84441;	
XX	DT 02-AUG-2003 (first entry)	
XX	DE Human secreted/transmembrane protein (PRO) #179.	
XX	KW Human; secreted and transmembrane protein; PRO; TNF-alpha;	
KW	tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;	
KW	tissue typing.	
XX	OS Homo sapiens.	
XX	PN US2003032112-A1.	
XX	PD 13-FEB-2003.	
XX	PF 21-JUN-2002; 2002US-00176756.	
XX	PR 18-SEP-1997; 97US-0059263P.	
PR	18-SEP-1997; 97US-0059266P.	
PR	17-OCT-1997; 97US-0062250P.	
PR	21-OCT-1997; 97US-0063486P.	
PR	24-OCT-1997; 97US-0063120P.	
PR	24-OCT-1997; 97US-0063121P.	
PR	28-OCT-1997; 97US-0063540P.	
PR	28-OCT-1997; 97US-0063541P.	
PR	28-OCT-1997; 97US-0063544P.	
PR	28-OCT-1997; 97US-0063564P.	
PR	29-OCT-1997; 97US-0063734P.	
PR	31-OCT-1997; 97US-0063870P.	

PR	31-OCT-1997;	97US-0064103P.
PR	13-NOV-1997;	97US-0065311P.
PR	21-NOV-1997;	97US-0066120P.
PR	24-NOV-1997;	97US-0066466P.
PR	24-NOV-1997;	97US-0066772P.
PR	11-DEC-1997;	97US-0069335P.
PR	12-DEC-1997;	97US-0069425P.
PR	17-DEC-1997;	97US-0069870P.
PR	18-DEC-1997;	97US-0068017P.
PR	10-MAR-1998;	98US-0077450P.
PR	11-MAR-1998;	98US-0077632P.
PR	11-MAR-1998;	98US-0077649P.
PR	20-MAR-1998;	98US-0078886P.
PR	20-MAR-1998;	98US-0078939P.
PR	27-MAR-1998;	98US-0079664P.
PR	27-MAR-1998;	98US-0079786P.
PR	31-MAR-1998;	98US-0080107P.
PR	31-MAR-1998;	98US-0080194P.
PR	01-APR-1998;	98US-0080327P.
PR	01-APR-1998;	98US-0080333P.
PR	08-APR-1998;	98US-0081049P.
PR	08-APR-1998;	98US-0081070P.
PR	09-APR-1998;	98US-0081195P.
PR	15-APR-1998;	98US-0081838P.
PR	21-APR-1998;	98US-0082568P.
PR	21-APR-1998;	98US-0082569P.
PR	22-APR-1998;	98US-0082704P.
PR	22-APR-1998;	98US-0082797P.
PR	28-APR-1998;	98US-0083322P.
PR	29-APR-1998;	98US-0083495P.
PR	29-APR-1998;	98US-0083496P.
PR	29-APR-1998;	98US-0083499P.
PR	29-APR-1998;	98US-0083559P.
PR	05-MAY-1998;	98US-0084366P.
PR	06-MAY-1998;	98US-0084414P.
PR	07-MAY-1998;	98US-0084639P.
PR	07-MAY-1998;	98US-0084640P.
PR	07-MAY-1998;	98US-0084643P.
PR	15-MAY-1998;	98US-0085579P.
PR	15-MAY-1998;	98US-0085580P.
PR	15-MAY-1998;	98US-0085582P.
PR	15-MAY-1998;	98US-0085700P.
PR	18-MAY-1998;	98US-0086023P.
PR	22-MAY-1998;	98US-0086392P.
PR	22-MAY-1998;	98US-0086486P.
PR	28-MAY-1998;	98US-0087098P.
PR	28-MAY-1998;	98US-0087208P.
PR	02-JUN-1998;	98US-0087609P.
PR	02-JUN-1998;	98US-0087759P.
PR	03-JUN-1998;	98US-0087827P.
PR	04-JUN-1998;	98US-0088025P.
PR	04-JUN-1998;	98US-0088028P.
PR	04-JUN-1998;	98US-0088029P.
PR	04-JUN-1998;	98US-0088033P.
PR	04-JUN-1998;	98US-0088326P.
PR	05-JUN-1998;	98US-0088167P.
PR	05-JUN-1998;	98US-0088202P.
PR	05-JUN-1998;	98US-0088212P.
PR	05-JUN-1998;	98US-0088217P.
PR	09-JUN-1998;	98US-0088655P.
PR	10-JUN-1998;	98US-0088722P.
PR	10-JUN-1998;	98US-0088738P.
PR	10-JUN-1998;	98US-0088740P.
PR	10-JUN-1998;	98US-0088811P.
PR	10-JUN-1998;	98US-0088824P.
PR	10-JUN-1998;	98US-0088825P.
PR	10-JUN-1998;	98US-0088826P.
PR	11-JUN-1998;	98US-0088861P.
PR	11-JUN-1998;	98US-0088863P.
PR	11-JUN-1998;	98US-0088876P.
PR	12-JUN-1998;	98US-0089090P.
PR	12-JUN-1998;	98US-0089105P.
PR	16-JUN-1998;	98US-0089512P.

PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090540P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091632P.
PR 24-JUL-1998; 98US-0094006P.
PR 04-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-0095998P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0097022P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0098014P.
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099602P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099812P.
PR 15-SEP-1998; 98US-0100388P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.

PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101477P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101922P.
PR 25-SEP-1998; 98US-0101786P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-00168978.

Query Match 100.0%; Score 225; DB 6; Length 225;
Best Local Similarity 100.0%; Pred. No. 3.2e-212;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNIIVVFENFWEGLMNCVRQANI 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNIIVVFENFWEGLMNCVRQANI 60

QY 61 RMOCKIYDSSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 RMOCKIYDSSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120

QY 121 TAGIIFIITGMVWLIPVSWANAIIRDfYNSIVNVAQKRELGEALYLGWTTALVLIIVGGA 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 TAGIIFIITGMVWLIPVSWANAIIRDfYNSIVNVAQKRELGEALYLGWTTALVLIIVGGA 180

QY 181 LFCCVFCCKNEKSSSYRYSIPSHRRTTQKSYHTGKSPSVYSRSQYV 225
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 LFCCVFCCKNEKSSSYRYSIPSHRRTTQKSYHTGKSPSVYSRSQYV 225

RESULT 11
ABR66315
ID ABR66315 standard; protein; 225 AA.
XX
AC ABR66315;
XX
DT 05-AUG-2003 (first entry)
XX
DE Human secreted polypeptide PRO1573, SEQ ID NO:358.
XX
KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnerary; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003027278-A1.
XX
PD 06-FEB-2003.
XX
PF 21-JUN-2002; 2002US-00176987.
XX
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.

us-10-063-732-120.olig6.rag

Fri Sep 3 10:15:53 2004

PR	21-OCT-1997;	97US-0063486P.	PR	10-JUN-1998;	98US-0088824P.
PR	24-OCT-1997;	97US-0063120P.	PR	10-JUN-1998;	98US-0088825P.
PR	24-OCT-1997;	97US-0063121P.	PR	10-JUN-1998;	98US-0088826P.
PR	28-OCT-1997;	97US-0063540P.	PR	11-JUN-1998;	98US-0088861P.
PR	28-OCT-1997;	97US-0063541P.	PR	11-JUN-1998;	98US-0088863P.
PR	28-OCT-1997;	97US-0063544P.	PR	11-JUN-1998;	98US-0088876P.
PR	28-OCT-1997;	97US-0063564P.	PR	12-JUN-1998;	98US-0089090P.
PR	29-OCT-1997;	97US-0063734P.	PR	12-JUN-1998;	98US-0089105P.
PR	31-OCT-1997;	97US-0063870P.	PR	16-JUN-1998;	98US-0089512P.
PR	31-OCT-1997;	97US-0064103P.	PR	16-JUN-1998;	98US-0089514P.
PR	13-NOV-1997;	97US-0065311P.	PR	17-JUN-1998;	98US-0089538P.
PR	21-NOV-1997;	97US-0066120P.	PR	17-JUN-1998;	98US-0089598P.
PR	24-NOV-1997;	97US-0066466P.	PR	17-JUN-1998;	98US-0089653P.
PR	24-NOV-1997;	97US-0066772P.	PR	18-JUN-1998;	98US-0089908P.
PR	11-DEC-1997;	97US-0069335P.	PR	19-JUN-1998;	98US-0089952P.
PR	12-DEC-1997;	97US-0069425P.	PR	22-JUN-1998;	98US-0090246P.
PR	17-DEC-1997;	97US-0069870P.	PR	22-JUN-1998;	98US-0090252P.
PR	18-DEC-1997;	97US-0068017P.	PR	22-JUN-1998;	98US-0090254P.
PR	10-MAR-1998;	98US-0077450P.	PR	24-JUN-1998;	98US-0090429P.
PR	11-MAR-1998;	98US-0077632P.	PR	24-JUN-1998;	98US-0090435P.
PR	11-MAR-1998;	98US-0077649P.	PR	24-JUN-1998;	98US-0090444P.
PR	20-MAR-1998;	98US-0078886P.	PR	24-JUN-1998;	98US-0090461P.
PR	20-MAR-1998;	98US-0078939P.	PR	24-JUN-1998;	98US-0090535P.
PR	27-MAR-1998;	98US-0079664P.	PR	24-JUN-1998;	98US-0090540P.
PR	27-MAR-1998;	98US-0079786P.	PR	25-JUN-1998;	98US-0090676P.
PR	31-MAR-1998;	98US-0080107P.	PR	25-JUN-1998;	98US-0090678P.
PR	31-MAR-1998;	98US-0080194P.	PR	25-JUN-1998;	98US-0090688P.
PR	01-APR-1998;	98US-0080327P.	PR	25-JUN-1998;	98US-0090690P.
PR	01-APR-1998;	98US-0080333P.	PR	25-JUN-1998;	98US-0090694P.
PR	08-APR-1998;	98US-0081049P.	PR	25-JUN-1998;	98US-0090695P.
PR	08-APR-1998;	98US-0081070P.	PR	25-JUN-1998;	98US-0090696P.
PR	09-APR-1998;	98US-0081195P.	PR	26-JUN-1998;	98US-00105413.
PR	15-APR-1998;	98US-0081838P.	PR	26-JUN-1998;	98US-0090862P.
PR	21-APR-1998;	98US-0082568P.	PR	26-JUN-1998;	98US-0090863P.
PR	21-APR-1998;	98US-0082569P.	PR	26-JUN-1998;	98US-0091010P.
PR	22-APR-1998;	98US-0082704P.	PR	01-JUL-1998;	98US-0091359P.
PR	22-APR-1998;	98US-0082797P.	PR	01-JUL-1998;	98US-0091544P.
PR	28-APR-1998;	98US-0083322P.	PR	02-JUL-1998;	98US-0091478P.
PR	29-APR-1998;	98US-0083495P.	PR	02-JUL-1998;	98US-0091486P.
PR	29-APR-1998;	98US-0083496P.	PR	02-JUL-1998;	98US-0091626P.
PR	29-APR-1998;	98US-0083499P.	PR	02-JUL-1998;	98US-0091628P.
PR	29-APR-1998;	98US-0083559P.	PR	02-JUL-1998;	98US-0091632P.
PR	05-MAY-1998;	98US-0084366P.	PR	24-JUL-1998;	98US-0094006P.
PR	06-MAY-1998;	98US-0084414P.	PR	04-AUG-1998;	98US-0095282P.
PR	07-MAY-1998;	98US-0084639P.	PR	10-AUG-1998;	98US-0095998P.
PR	07-MAY-1998;	98US-0084640P.	PR	10-AUG-1998;	98US-0096012P.
PR	07-MAY-1998;	98US-0084643P.	PR	17-AUG-1998;	98US-0096757P.
PR	15-MAY-1998;	98US-0085579P.	PR	17-AUG-1998;	98US-0096766P.
PR	15-MAY-1998;	98US-0085580P.	PR	17-AUG-1998;	98US-0096867P.
PR	15-MAY-1998;	98US-0085582P.	PR	17-AUG-1998;	98US-0096891P.
PR	15-MAY-1998;	98US-0085700P.	PR	17-AUG-1998;	98US-0096897P.
PR	18-MAY-1998;	98US-0086023P.	PR	18-AUG-1998;	98US-0096949P.
PR	22-MAY-1998;	98US-0086392P.	PR	18-AUG-1998;	98US-0096959P.
PR	22-MAY-1998;	98US-0086486P.	PR	26-AUG-1998;	98US-0097022P.
PR	28-MAY-1998;	98US-0087098P.	PR	26-AUG-1998;	98US-0097952P.
PR	28-MAY-1998;	98US-0087208P.	PR	26-AUG-1998;	98US-0097954P.
PR	02-JUN-1998;	98US-0087609P.	PR	26-AUG-1998;	98US-0097955P.
PR	03-JUN-1998;	98US-0087759P.	PR	26-AUG-1998;	98US-0097971P.
PR	04-JUN-1998;	98US-0087827P.	PR	26-AUG-1998;	98US-0097974P.
PR	04-JUN-1998;	98US-0088025P.	PR	26-AUG-1998;	98US-0098014P.
PR	04-JUN-1998;	98US-0088028P.	PR	01-SEP-1998;	98US-0098716P.
PR	04-JUN-1998;	98US-0088029P.	PR	01-SEP-1998;	98US-0098723P.
PR	04-JUN-1998;	98US-0088033P.	PR	02-SEP-1998;	98US-0098803P.
PR	04-JUN-1998;	98US-0088326P.	PR	02-SEP-1998;	98US-0098821P.
PR	05-JUN-1998;	98US-0088167P.	PR	02-SEP-1998;	98US-0098843P.
PR	05-JUN-1998;	98US-0088202P.	PR	09-SEP-1998;	98US-0099602P.
PR	05-JUN-1998;	98US-0088212P.	PR	10-SEP-1998;	98US-0099741P.
PR	09-JUN-1998;	98US-0088217P.	PR	10-SEP-1998;	98US-0099754P.
PR	10-JUN-1998;	98US-0088655P.	PR	10-SEP-1998;	98US-0099763P.
PR	10-JUN-1998;	98US-0088722P.	PR	10-SEP-1998;	98US-0099812P.
PR	10-JUN-1998;	98US-0088738P.	PR	15-SEP-1998;	98US-0100388P.
PR	10-JUN-1998;	98US-0088740P.	PR	16-SEP-1998;	98US-0100662P.
PR	10-JUN-1998;	98US-0088811P.	PR	16-SEP-1998;	98US-0100664P.

PR	16-SEP-1998;	98US-0101751P.	PR	16-SEP-1998;	2002US-00188773.
PR	16-SEP-1998;	98WO-US019330.	XX		
PR	17-SEP-1998;	98US-0100683P.	PR	18-SEP-1997;	97US-0059263P.
PR	17-SEP-1998;	98US-0100684P.	PR	18-SEP-1997;	97US-0059266P.
PR	17-SEP-1998;	98US-0100919P.	PR	17-OCT-1997;	97US-0062250P.
PR	17-SEP-1998;	98US-0100930P.	PR	21-OCT-1997;	97US-0063486P.
PR	18-SEP-1998;	98US-0100849P.	PR	24-OCT-1997;	97US-0063120P.
PR	18-SEP-1998;	98US-0101014P.	PR	24-OCT-1997;	97US-0063121P.
PR	18-SEP-1998;	98US-0101068P.	PR	28-OCT-1997;	97US-0063540P.
PR	23-SEP-1998;	98US-0101471P.	PR	28-OCT-1997;	97US-0063541P.
PR	23-SEP-1998;	98US-0101472P.	PR	28-OCT-1997;	97US-0063544P.
PR	23-SEP-1998;	98US-0101475P.	PR	28-OCT-1997;	97US-0063564P.
PR	23-SEP-1998;	98US-0101477P.	PR	29-OCT-1997;	97US-0063734P.
PR	24-SEP-1998;	98US-0101738P.	PR	31-OCT-1997;	97US-0063870P.
PR	24-SEP-1998;	98US-0101739P.	PR	31-OCT-1997;	97US-0064103P.
PR	24-SEP-1998;	98US-0101743P.	PR	13-NOV-1997;	97US-0065311P.
PR	24-SEP-1998;	98US-0101922P.	PR	21-NOV-1997;	97US-0066120P.
PR	25-SEP-1998;	98US-0101786P.	PR	24-NOV-1997;	97US-0066466P.
PR	29-SEP-1998;	98US-0102207P.	PR	24-NOV-1997;	97US-0066772P.
PR	29-SEP-1998;	98US-0102240P.	PR	11-DEC-1997;	97US-0069335P.
PR	29-SEP-1998;	98US-0102330P.	PR	12-DEC-1997;	97US-0069425P.
PR	29-SEP-1998;	98US-0102331P.	PR	17-DEC-1997;	97US-0069870P.
PR	30-SEP-1998;	98US-0102487P.	PR	18-DEC-1997;	97US-0068017P.
PR	30-SEP-1998;	98US-0102570P.	PR	10-MAR-1998;	98US-0077450P.
PR	30-SEP-1998;	98US-0102571P.	PR	11-MAR-1998;	98US-0077632P.
PR	01-OCT-1998;	98US-0102684P.	PR	11-MAR-1998;	98US-0077649P.
PR	01-OCT-1998;	98US-0102687P.	PR	20-MAR-1998;	98US-0078886P.
Query Match 100.0%; Score 225; DB 6; Length 225;			PR	20-MAR-1998;	98US-0078939P.
Best Local Similarity 100.0%; Pred. No. 3.2e-212;			PR	27-MAR-1998;	98US-0079664P.
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			PR	27-MAR-1998;	98US-0079786P.
QY	1	MATHALEIAGFLGGVGMGTVAVTMPQWRVS	PR	31-MAR-1998;	98US-0080107P.
		AFIENNIIVVFENFWEGLMNCVRQANI 60	PR	31-MAR-1998;	98US-0080194P.
Db	1	MATHALEIAGFLGGVGMGTVAVTMPQWRVS	PR	01-APR-1998;	98US-0080327P.
		AFIENNIIVVFENFWEGLMNCVRQANI 60	PR	01-APR-1998;	98US-0080333P.
QY	61	RMOCKIYDSSLALSPDLQAARGLMCAASVMS	PR	08-APR-1998;	98US-0081049P.
		FLAFMAILGKCTRCTGDNEKVAHILL 120	PR	08-APR-1998;	98US-0081070P.
Db	61	RMOCKIYDSSLALSPDLQAARGLMCAASVMS	PR	09-APR-1998;	98US-0081195P.
		FLAFMAILGKCTRCTGDNEKVAHILL 120	PR	15-APR-1998;	98US-0081838P.
QY	121	TAGIIFIITGMVVLIPVSWANAIIRD	PR	21-APR-1998;	98US-0082568P.
		FYNSIVNVAQKRELGEALYLGTTALVLI	PR	21-APR-1998;	98US-0082569P.
Db	121	TAGIIFIITGMVVLIPVSWANAIIRD	PR	22-APR-1998;	98US-0082704P.
		FYNSIVNVAQKRELGEALYLGTTALVLI	PR	22-APR-1998;	98US-0082797P.
QY	181	LFCCVFCCKNEKSSSYRYSIPSHRTTQKSY	PR	28-APR-1998;	98US-0083322P.
		HTGKSPSVYRSQYV 225	PR	29-APR-1998;	98US-0083495P.
Db	181	LFCCVFCCKNEKSSSYRYSIPSHRTTQKSY	PR	29-APR-1998;	98US-0083496P.
		HTGKSPSVYRSQYV 225	PR	29-APR-1998;	98US-0083499P.
RESULT 12			PR	29-APR-1998;	98US-0083559P.
ABR65705			PR	05-MAY-1998;	98US-0084366P.
ID	ABR65705 standard; protein; 225 AA.		PR	06-MAY-1998;	98US-0084414P.
XX			PR	07-MAY-1998;	98US-0084639P.
AC	ABR65705;		PR	07-MAY-1998;	98US-0084640P.
XX			PR	07-MAY-1998;	98US-0084643P.
DT	05-AUG-2003 (first entry)		PR	15-MAY-1998;	98US-0085579P.
XX			PR	15-MAY-1998;	98US-0085580P.
DE	Human secreted polypeptide PRO1573, SEQ ID NO:358.		PR	15-MAY-1998;	98US-0085582P.
XX			PR	15-MAY-1998;	98US-0085700P.
KW	Human; PRO; secreted protein; transmembrane protein;		PR	18-MAY-1998;	98US-0086023P.
KW	extracellular domain; tumour necrosis factor-alpha; TNF-alpha;		PR	22-MAY-1998;	98US-0086392P.
KW	chondrocyte; proliferation; differentiation; cartilage disorder;		PR	22-MAY-1998;	98US-0086486P.
KW	bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;		PR	28-MAY-1998;	98US-0087098P.
KW	adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;		PR	28-MAY-1998;	98US-0087208P.
KW	liver; drug screening; transgenic animal; genetic analysis;		PR	02-JUN-1998;	98US-0087609P.
KW	antiarthritic; vulneryary; gene therapy.		PR	02-JUN-1998;	98US-0087759P.
XX			PR	03-JUN-1998;	98US-0087827P.
OS	Homo sapiens.		PR	04-JUN-1998;	98US-0088025P.
XX			PR	04-JUN-1998;	98US-0088028P.
PN	US2003036159-A1.		PR	04-JUN-1998;	98US-0088033P.
XX			PR	04-JUN-1998;	98US-0088326P.
XX			PR	05-JUN-1998;	98US-0088167P.
PD	20-FEB-2003.		PR	05-JUN-1998;	98US-0088202P.
XX			PR	05-JUN-1998;	98US-0088212P.
			PR	05-JUN-1998;	98US-0088217P.

PR	09-JUN-1998;	98US-0088655P.	PR	10-SEP-1998;	98US-0099763P.
PR	10-JUN-1998;	98US-0088722P.	PR	10-SEP-1998;	98US-0099812P.
PR	10-JUN-1998;	98US-0088738P.	PR	15-SEP-1998;	98US-0100388P.
PR	10-JUN-1998;	98US-0088740P.	PR	16-SEP-1998;	98US-0100662P.
PR	10-JUN-1998;	98US-0088811P.	PR	16-SEP-1998;	98US-0100664P.
PR	10-JUN-1998;	98US-0088824P.	PR	16-SEP-1998;	98US-0101751P.
PR	10-JUN-1998;	98US-0088825P.	PR	16-SEP-1998;	98WO-US019330.
PR	10-JUN-1998;	98US-0088826P.	PR	17-SEP-1998;	98US-0100683P.
PR	11-JUN-1998;	98US-0088861P.	PR	17-SEP-1998;	98US-0100684P.
PR	11-JUN-1998;	98US-0088863P.	PR	17-SEP-1998;	98US-0100919P.
PR	11-JUN-1998;	98US-0088876P.	PR	17-SEP-1998;	98US-0100930P.
PR	12-JUN-1998;	98US-0089090P.	PR	18-SEP-1998;	98US-0100849P.
PR	12-JUN-1998;	98US-0089105P.	PR	18-SEP-1998;	98US-0101014P.
PR	16-JUN-1998;	98US-0089512P.	PR	18-SEP-1998;	98US-0101068P.
PR	16-JUN-1998;	98US-0089514P.	PR	23-SEP-1998;	98US-0101471P.
PR	17-JUN-1998;	98US-0089538P.	PR	23-SEP-1998;	98US-0101472P.
PR	17-JUN-1998;	98US-0089598P.	PR	23-SEP-1998;	98US-0101475P.
PR	17-JUN-1998;	98US-0089653P.	PR	23-SEP-1998;	98US-0101477P.
PR	18-JUN-1998;	98US-0089908P.	PR	24-SEP-1998;	98US-0101738P.
PR	19-JUN-1998;	98US-0089952P.	PR	24-SEP-1998;	98US-0101739P.
PR	22-JUN-1998;	98US-0090246P.	PR	24-SEP-1998;	98US-0101743P.
PR	22-JUN-1998;	98US-0090252P.	PR	24-SEP-1998;	98US-0101922P.
PR	22-JUN-1998;	98US-0090254P.	PR	25-SEP-1998;	98US-0101786P.
PR	24-JUN-1998;	98US-0090429P.	PR	29-SEP-1998;	98US-0102207P.
PR	24-JUN-1998;	98US-0090435P.	PR	29-SEP-1998;	98US-0102240P.
PR	24-JUN-1998;	98US-0090444P.	PR	29-SEP-1998;	98US-0102330P.
PR	24-JUN-1998;	98US-0090461P.	PR	29-SEP-1998;	98US-0102331P.
PR	24-JUN-1998;	98US-0090535P.	PR	30-SEP-1998;	98US-0102487P.
PR	24-JUN-1998;	98US-0090540P.	PR	30-SEP-1998;	98US-0102570P.
PR	25-JUN-1998;	98US-0090676P.	PR	30-SEP-1998;	98US-0102571P.
PR	25-JUN-1998;	98US-0090678P.	PR	01-OCT-1998;	98US-0102684P.
PR	25-JUN-1998;	98US-0090688P.	PR	01-OCT-1998;	98US-0102687P.
PR	25-JUN-1998;	98US-0090690P.			
PR	25-JUN-1998;	98US-0090694P.			
PR	25-JUN-1998;	98US-0090695P.			
PR	25-JUN-1998;	98US-0090696P.			
PR	26-JUN-1998;	98US-00105413.			
PR	26-JUN-1998;	98US-0090862P.			
PR	26-JUN-1998;	98US-0090863P.			
PR	26-JUN-1998;	98US-0091010P.			
PR	01-JUL-1998;	98US-0091359P.			
PR	01-JUL-1998;	98US-0091544P.			
PR	02-JUL-1998;	98US-0091478P.			
PR	02-JUL-1998;	98US-0091486P.			
PR	02-JUL-1998;	98US-0091626P.			
PR	02-JUL-1998;	98US-0091628P.			
PR	02-JUL-1998;	98US-0091632P.			
PR	24-JUL-1998;	98US-0094006P.			
PR	04-AUG-1998;	98US-0095282P.			
PR	10-AUG-1998;	98US-0095998P.			
PR	10-AUG-1998;	98US-0096012P.			
PR	17-AUG-1998;	98US-0096757P.			
PR	17-AUG-1998;	98US-0096766P.			
PR	17-AUG-1998;	98US-0096867P.			
PR	17-AUG-1998;	98US-0096891P.			
PR	17-AUG-1998;	98US-0096897P.			
PR	18-AUG-1998;	98US-0096949P.			
PR	18-AUG-1998;	98US-0096959P.			
PR	18-AUG-1998;	98US-0097022P.			
PR	26-AUG-1998;	98US-0097952P.			
PR	26-AUG-1998;	98US-0097954P.			
PR	26-AUG-1998;	98US-0097955P.			
PR	26-AUG-1998;	98US-0097971P.			
PR	26-AUG-1998;	98US-0097974P.			
PR	26-AUG-1998;	98US-0098014P.			
PR	01-SEP-1998;	98US-0098716P.			
PR	01-SEP-1998;	98US-0098723P.			
PR	02-SEP-1998;	98US-0098803P.			
PR	02-SEP-1998;	98US-0098821P.			
PR	02-SEP-1998;	98US-0098843P.			
PR	09-SEP-1998;	98US-0099602P.			
PR	10-SEP-1998;	98US-0099741P.			
PR	10-SEP-1998;	98US-0099754P.			
QY	1	MATHALEIAGLFLGGVGMGTVAVTMPQWRVSAFIENNIIVVFENFWEGLWMNCVROANI	60		
Db	1	MATHALEIAGLFLGGVGMGTVAVTMPQWRVSAFIENNIIVVFENFWEGLWMNCVROANI	60		
QY	61	RMQCKIYDSLALSPDLQAARGLMCAASVMSFLAFMAILGKCTRCTGDNEKVKAHILL	120		
Db	61	RMQCKIYDSLALSPDLQAARGLMCAASVMSFLAFMAILGKCTRCTGDNEKVKAHILL	120		
QY	121	TAGIIFIITGMVVLIPVSVWANAIIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGA	180		
Db	121	TAGIIFIITGMVVLIPVSVWANAIIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGA	180		
QY	181	LFCCVFCCNEKSSSYRYSIPSHRTTQKSQYHTGKSPSVYRSQYV	225		
Db	181	LFCCVFCCNEKSSSYRYSIPSHRTTQKSQYHTGKSPSVYRSQYV	225		
RESULT 13					
ABU99645					
ID	ABU99645 standard; protein; 225 AA.				
XX	AC ABU99645;				
XX	DT 09-AUG-2003 (first entry)				
XX	Human secreted/transmembrane protein (PRO) #179.				
XX	Human; secreted and transmembrane protein; PRO; TNF-alpha;				
KW	tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;				
KW	tissue typing.				
XX	Homo sapiens.				
OS	US2003040070-A1.				
XX	27-FEB-2003.				
PD					
Query Match 100.0%; Score 225; DB 6; Length 225;					
Best Local Similarity 100.0%; Pred. No. 3.2e-212;					
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					

XX	27-JUN-2002;	2002US-00184627.	
PF	18-SEP-1997;	97US-0059263P.	05-JUN-1998;
XX	18-SEP-1997;	97US-0059266P.	PR
PR	17-OCT-1997;	97US-0062250P.	PR
PR	21-OCT-1997;	97US-0063486P.	PR
PR	24-OCT-1997;	97US-0063120P.	PR
PR	24-OCT-1997;	97US-0063121P.	PR
PR	28-OCT-1997;	97US-0063540P.	PR
PR	28-OCT-1997;	97US-0063541P.	PR
PR	28-OCT-1997;	97US-0063544P.	PR
PR	28-OCT-1997;	97US-0063564P.	PR
PR	29-OCT-1997;	97US-0063734P.	PR
PR	31-OCT-1997;	97US-0063870P.	PR
PR	31-OCT-1997;	97US-0064103P.	PR
PR	13-NOV-1997;	97US-0065311P.	PR
PR	21-NOV-1997;	97US-0066120P.	PR
PR	24-NOV-1997;	97US-0066466P.	PR
PR	24-NOV-1997;	97US-0066772P.	PR
PR	11-DEC-1997;	97US-0069335P.	PR
PR	12-DEC-1997;	97US-0069425P.	PR
PR	17-DEC-1997;	97US-0069870P.	PR
PR	18-DEC-1997;	97US-0068017P.	PR
PR	10-MAR-1998;	98US-0077450P.	PR
PR	11-MAR-1998;	98US-0077632P.	PR
PR	11-MAR-1998;	98US-0077649P.	PR
PR	20-MAR-1998;	98US-0078886P.	PR
PR	20-MAR-1998;	98US-0078939P.	PR
PR	27-MAR-1998;	98US-0079664P.	PR
PR	27-MAR-1998;	98US-0079786P.	PR
PR	31-MAR-1998;	98US-0080107P.	PR
PR	31-MAR-1998;	98US-0080194P.	PR
PR	01-APR-1998;	98US-0080327P.	PR
PR	01-APR-1998;	98US-0080333P.	PR
PR	08-APR-1998;	98US-0081049P.	PR
PR	08-APR-1998;	98US-0081070P.	PR
PR	09-APR-1998;	98US-0081195P.	PR
PR	15-APR-1998;	98US-0081838P.	PR
PR	21-APR-1998;	98US-0082568P.	PR
PR	21-APR-1998;	98US-0082569P.	PR
PR	22-APR-1998;	98US-0082704P.	PR
PR	22-APR-1998;	98US-0082797P.	PR
PR	28-APR-1998;	98US-0083322P.	PR
PR	29-APR-1998;	98US-0083495P.	PR
PR	29-APR-1998;	98US-0083496P.	PR
PR	29-APR-1998;	98US-0083499P.	PR
PR	29-APR-1998;	98US-0083559P.	PR
PR	05-MAY-1998;	98US-0084366P.	PR
PR	06-MAY-1998;	98US-0084414P.	PR
PR	07-MAY-1998;	98US-0084639P.	PR
PR	07-MAY-1998;	98US-0084640P.	PR
PR	07-MAY-1998;	98US-0084643P.	PR
PR	15-MAY-1998;	98US-0085579P.	PR
PR	15-MAY-1998;	98US-0085580P.	PR
PR	15-MAY-1998;	98US-0085582P.	PR
PR	15-MAY-1998;	98US-0085700P.	PR
PR	18-MAY-1998;	98US-0086023P.	PR
PR	22-MAY-1998;	98US-0086392P.	PR
PR	22-MAY-1998;	98US-0086486P.	PR
PR	28-MAY-1998;	98US-0087098P.	PR
PR	28-MAY-1998;	98US-0087208P.	PR
PR	02-JUN-1998;	98US-0087609P.	PR
PR	02-JUN-1998;	98US-0087759P.	PR
PR	03-JUN-1998;	98US-0087827P.	PR
PR	04-JUN-1998;	98US-0088025P.	PR
PR	04-JUN-1998;	98US-0088028P.	PR
PR	04-JUN-1998;	98US-0088029P.	PR
PR	04-JUN-1998;	98US-0088033P.	PR
PR	04-JUN-1998;	98US-0088326P.	PR
PR	05-JUN-1998;	98US-0088167P.	PR
PR	05-JUN-1998;	98US-0088202P.	PR
PR	05-JUN-1998;	98US-0088212P.	PR
PR	05-JUN-1998;	98US-0088217P.	PR
PR	09-JUN-1998;	98US-0088655P.	PR
PR	10-JUN-1998;	98US-0088656P.	PR
PR	10-JUN-1998;	98US-0088722P.	PR
PR	10-JUN-1998;	98US-0088738P.	PR
PR	10-JUN-1998;	98US-0088740P.	PR
PR	10-JUN-1998;	98US-0088811P.	PR
PR	10-JUN-1998;	98US-0088824P.	PR
PR	10-JUN-1998;	98US-0088825P.	PR
PR	10-JUN-1998;	98US-0088826P.	PR
PR	11-JUN-1998;	98US-0088861P.	PR
PR	11-JUN-1998;	98US-0088863P.	PR
PR	11-JUN-1998;	98US-0088876P.	PR
PR	12-JUN-1998;	98US-0089090P.	PR
PR	12-JUN-1998;	98US-0089105P.	PR
PR	16-JUN-1998;	9	

Fri Sep 3 10:15:53 2004

us-10-063-732-120.olig6.rag

PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099812P.
PR 15-SEP-1998; 98US-0100388P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101477P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101922P.
PR 25-SEP-1998; 98US-0101786P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-00168978.

Query Match 100.0%; Score 225; DB 6; Length 225;
Best Local Similarity 100.0%; Pred. No. 3.2e-212;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATHALEIAGFLGGVGMVGTAVTVMPPQWRVSAFIENNIIVFENFWEGLWMNCVRQANI 60
Db 1 MATHALEIAGFLGGVGMVGTAVTVMPPQWRVSAFIENNIIVFENFWEGLWMNCVRQANI 60
QY 61 RMQCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120
Db 61 RMQCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120
QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIYNVAQKRELGEALYLGWTTALVLIVGGA 180
Db 121 TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIYNVAQKRELGEALYLGWTTALVLIVGGA 180
QY 181 LFCCVFCCKNEKSSSYRYSIPSHRRTTQKSYHTGKKSPSVYRSQYV 225
Db 181 LFCCVFCCKNEKSSSYRYSIPSHRRTTQKSYHTGKKSPSVYRSQYV 225

RESULT 14
ABU82884
ID ABU82884 standard; protein; 225 AA.
XX AC ABU82884;
XX XX
DT 27-JUN-2003 (first entry)
XX XX
DE Human PRO polypeptide #179.
XX XX
KW Human; PRO polypeptide; secreted and transmembrane protein; tumour;
KW chromosome mapping; gene mapping; cytostatic.
XX XX
OS Homo sapiens.

XX US2003032113-A1.
PN 13-FEB-2003.
XX 20-JUN-2002; 2002US-00176911.
PD 18-SEP-1997; 97US-0059263P.
XX 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066772P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078939P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080333P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081838P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083559P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085700P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087208P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088033P.

XX Human; gene therapy; tissue typing; tumour; chondrocyte proliferation;
KW chondrocyte differentiation; tumour necrosis factor-alpha release;
KW affinity purification.
XX Homo sapiens.
OS
XX US2003036147-A1.
PN
XX
PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-00187741.
XX
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066772P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078939P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080333P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081838P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083559P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085700P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087208P.
PR 02-JUN-1998; 98US-0087609P.

PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090540P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091632P.
PR 24-JUL-1998; 98US-0094006P.
PR 04-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-0095998P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0097022P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.

[illegible]

Search completed: September 1, 2004, 16:58:20
Job time : 56 secs

Blank Set 15/17